STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 143069

TO: Terra Gibbs Location: REM-2D10&2C18 Art Unit: 1635 Wednesday, March 30, 2005 Case Serial Number: 09/888164	From: Barb O'Bryen Location: Biotech-Chem Library Remsen 1a69 Phone: 571-272-2518 BOB barbara.obryen@uspto.gov

Search Notes

STIC-Biotech/ChemLib 148369

From: Gibbs, Terra
Sent: Monday, March 21, 2005 2:46 PM
To: STIC-Biotech/ChemLib
Subject: sequence search request...

Please perform a search of SEQ ID NO:29 of USSN 09/888,164 in all commercial databases, pending files, and pre-grant pubs.
Please perform this search as:
a) a regular search for any sequences comprising SEQ ID NO:29 and
b) a length limited search wherein the length of the oligo hits is limited to less than 50 nucleotides in length.

CRF6

Terra Cotta Gibbs, Ph.D.
Art Unit 1635
Remsen Building 2D10
Mailbox 2C18
571-272-0758

****
STAFF USE ONLY

Searcher:_____
Searcher Phone: 2-
Date Searcher Picked up:____
Date Completed:_____
Searcher Prep/Rev. Time:___
Online Time:_____

****
Type of Search

NA#:_____ AA#:_____
Interference:____ SPDI:___
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure#:_____ Text:___
Inventor:____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other(Specify):_____

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 29, 2005, 03:27:51 ; Search time 1446 Seconds
(without alignments)
536.157 Million cell updates/sec

Title: US-09-888-164-29
Perfect score: 16
Sequence: 1 aaagccacccaaggca 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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2: gb_htg:*
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13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		16	100.0	16	6	A66874	A66874 Sequence 41
2		16	100.0	16	6	I55199	I55199 Sequence 48
3		16	100.0	16	6	AR271346	AR271346 Sequence
4		16	100.0	16	6	AR488376	AR488376 Sequence
5		16	100.0	18	6	A66882	A66882 Sequence 49
6		16	100.0	18	6	I65373	I65373 Sequence 22
7		16	100.0	18	6	AR488384	AR488384 Sequence
8	c	16	100.0	19	6	I65372	I65372 Sequence 21
9	c	16	100.0	19	6	I65376	I65376 Sequence 25
10	c	16	100.0	20	6	A18805	A18805 oligonucleo
11	c	16	100.0	20	6	A18806	A18806 oligonucleo
12		16	100.0	20	6	AR086981	AR086981 Sequence
13		16	100.0	20	6	E08672	E08672 PCR primer
14		16	100.0	21	6	AR086970	AR086970 Sequence
15		16	100.0	21	6	I55196	I55196 Sequence 45
16		16	100.0	21	6	I55198	I55198 Sequence 47
17		16	100.0	21	6	I92344	I92344 Sequence 5
18		16	100.0	21	6	AR271343	AR271343 Sequence
19		16	100.0	21	6	AR271345	AR271345 Sequence
20	c	16	100.0	23	6	A18804	A18804 oligonucleo
21	c	16	100.0	23	6	AR000182	AR000182 Sequence
22	c	16	100.0	23	6	E09725	E09725 Primer OAL4
23	c	16	100.0	23	6	AX250613	AX250613 Sequence
24	c	16	100.0	44	6	I65370	I65370 Sequence 19
25	c	16	100.0	44	6	I65371	I65371 Sequence 20
26	c	16	100.0	50	6	AR000194	AR000194 Sequence
27	c	16	100.0	61	6	AR279728	AR279728 Sequence
28	c	16	100.0	69	6	I23307	I23307 Sequence 10
29	c	16	100.0	72	6	AR028629	AR028629 Sequence
30	c	16	100.0	81	6	I92348	I92348 Sequence 9
31	c	16	100.0	87	6	E10006	E10006 Human HBV P
32	c	16	100.0	87	6	AX151115	AX151115 Sequence
33	c	16	100.0	87	14	HPBPREC	M33947 Hepatitis B
34	c	16	100.0	87	14	S64971	S64971 (G to A mut
35	c	16	100.0	90	14	S75619	S75619 precore reg
36	c	16	100.0	94	6	E12994	E12994 DNA encodin
37	c	16	100.0	94	6	E12995	E12995 DNA encodin
38	c	16	100.0	94	6	E12996	E12996 DNA encodin
39	c	16	100.0	94	6	E12997	E12997 DNA encodin
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42	c	16	100.0	99	14	HPBPRECC	M76689 Hepatitis B
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45	c	16	100.0	99	14	HPBPRECF	M76692 Hepatitis B

ALIGNMENTS

RESULT 1
A66874
LOCUS A66874 16 bp DNA linear PAT 29-MAR-1999
DEFINITION Sequence 41 from Patent WO9740193.
ACCESSION A66874
VERSION A66874.1 GI:4538245
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Stuyver,L., Rossau,R. and Maertens,G.
TITLE METHOD FOR TYPING AND DETECTING HBV
JOURNAL Patent: WO 9740193-A 41 30-OCT-1997;
INNOGENETICS NV (BE)
FEATURES Location/Qualifiers
source 1. .16
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/db_xref="taxon:32644"
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Query Match 100.0%; Score 16; DB 6; Length 16;
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAAGGCA 16
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Db 1 AAAGCCACCCAAGGCA 16

RESULT 2
I55199
LOCUS I55199 16 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 48 from patent US 5646262.
ACCESSION I55199
VERSION I55199.1 GI:2476402
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)

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  AUTHORS   Korba,B.E. and Gerin,J.L.
  TITLE     Antisense oligonucleotides against hepatitis B viral replication
  JOURNAL   Patent: US 5646262-A 48 08-JUL-1997;
FEATURES             Location/Qualifiers
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Db          1 AAAGCCACCCAAGGCA 16


RESULT 3
AR271346
LOCUS       AR271346                  16 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 48 from patent US 6503533.
ACCESSION   AR271346
VERSION     AR271346.1  GI:29702721
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Korba,B.E. and Gerin,J.L.
  TITLE     Antisense ogligonucleotides against Hepatitis B viral replication
  JOURNAL   Patent: US 6503533-A 48 07-JAN-2003;
FEATURES             Location/Qualifiers
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ORIGIN

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Qy          1 AAAGCCACCCAAGGCA 16
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Db          1 AAAGCCACCCAAGGCA 16


RESULT 4
AR488376
LOCUS       AR488376                  16 bp    DNA     linear   PAT 15-MAY-2004
DEFINITION  Sequence 41 from patent US 6709812.
ACCESSION   AR488376
VERSION     AR488376.1  GI:47254428
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Stuyver,L., Rossau,R. and Maertens,G.
  TITLE     Method for typing and detecting HBV
  JOURNAL   Patent: US 6709812-A 41 23-MAR-2004;
FEATURES             Location/Qualifiers
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Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 5
A66882
LOCUS       A66882                    18 bp    DNA     linear   PAT 29-MAR-1999
DEFINITION  Sequence 49 from Patent WO9740193.
ACCESSION   A66882
VERSION     A66882.1  GI:4538253
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Stuyver,L., Rossau,R. and Maertens,G.
  TITLE     METHOD FOR TYPING AND DETECTING HBV
  JOURNAL   Patent: WO 9740193-A 49 30-OCT-1997;
            INNOGENETICS NV (BE)
FEATURES             Location/Qualifiers
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ORIGIN

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Qy          1 AAAGCCACCCAAGGCA 16
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Db          1 AAAGCCACCCAAGGCA 16


RESULT 6
I65373
LOCUS       I65373                    18 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 22 from patent US 5667974.
ACCESSION   I65373
VERSION     I65373.1  GI:2481943
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Birkenmeyer,L. and Mushahwar,I.K.
  TITLE     Method for detecting nucleic acid sequences using competitive
            amplification
  JOURNAL   Patent: US 5667974-A 22 16-SEP-1997;
FEATURES             Location/Qualifiers
     source          1. .18
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Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 7
AR488384
LOCUS       AR488384                  18 bp    DNA     linear   PAT 15-MAY-2004
DEFINITION  Sequence 49 from patent US 6709812.
ACCESSION   AR488384
VERSION     AR488384.1  GI:47254436
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Stuyver,L., Rossau,R. and Maertens,G.
  TITLE     Method for typing and detecting HBV
  JOURNAL   Patent: US 6709812-A 49 23-MAR-2004;
FEATURES             Location/Qualifiers
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ORIGIN

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Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 8
I65372/c
LOCUS       I65372                    19 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 21 from patent US 5667974.
ACCESSION   I65372
VERSION     I65372.1  GI:2481942
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Birkenmeyer,L. and Mushahwar,I.K.
  TITLE     Method for detecting nucleic acid sequences using competitive
            amplification
  JOURNAL   Patent: US 5667974-A 21 16-SEP-1997;
FEATURES             Location/Qualifiers
     source          1. .19
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         18 AAAGCCACCCAAGGCA 3


RESULT 9
I65376/c
LOCUS       I65376                    19 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 25 from patent US 5667974.
ACCESSION   I65376
VERSION     I65376.1  GI:2481946
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Birkenmeyer,L. and Mushahwar,I.K.
  TITLE     Method for detecting nucleic acid sequences using competitive
            amplification
  JOURNAL   Patent: US 5667974-A 25 16-SEP-1997;
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Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         18 AAAGCCACCCAAGGCA 3


RESULT 10
A18805/c
LOCUS       A18805                    20 bp    DNA     linear   PAT 22-APR-1994
DEFINITION  oligonucleotide primer.
ACCESSION   A18805
VERSION     A18805.1  GI:513426
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   .
  TITLE     PROGNOSIS OF HEPATITIS INFECTION
  JOURNAL   Patent: WO 9114789-A 2 03-OCT-1991;
FEATURES             Location/Qualifiers
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ORIGIN

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Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         19 AAAGCCACCCAAGGCA 4


RESULT 11
A18806/c
LOCUS       A18806                    20 bp    DNA     linear   PAT 22-APR-1994
DEFINITION  oligonucleotide primer.
ACCESSION   A18806
VERSION     A18806.1  GI:513427
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   .
  TITLE     PROGNOSIS OF HEPATITIS INFECTION
  JOURNAL   Patent: WO 9114789-A 3 03-OCT-1991;
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Db         19 AAAGCCACCCAAGGCA 4


RESULT 12
AR086981
LOCUS       AR086981                  20 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 18 from patent US 5985662.
ACCESSION   AR086981
VERSION     AR086981.1  GI:10013747
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Anderson,K.P. and Cowsert,L.M.
  TITLE     Antisense inhibition of hepatitis B virus replication
  JOURNAL   Patent: US 5985662-A 18 16-NOV-1999;
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Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 13
E08672
LOCUS       E08672                    20 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  PCR primer for gaining polypeptide from X protein of Hepatitis B
            virus.
ACCESSION   E08672
VERSION     E08672.1  GI:2176785
KEYWORDS    JP 1995033797-A/5.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Uchida,T. and Shikata,T.
  TITLE     HEPATITIS B VIRUS-DERIVED POLYPEPTIDE AND GENE CODING THE SAME
            POLYPEPTIDE
  JOURNAL   Patent: JP 1995033797-A 5 03-FEB-1995;
            MITSUBISHI CHEM CORP
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1995033797-A/5
            PD   03-FEB-1995
            PF   21-JUL-1993 JP 1993180314
            PI   UCHIDA TOSHIKAZU, SHIKATA TOSHIO
            PC   C07K14/02,C12N15/09,C12P21/02,G01N33/53,G01N33/569,G01N33/576;
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            CC   topology: Linear;
            CC   hypothetical: No;
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Db          3 AAAGCCACCCAAGGCA 18


RESULT 14
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LOCUS       AR086970                  21 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 7 from patent US 5985662.
ACCESSION   AR086970
VERSION     AR086970.1  GI:10013736
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Anderson,K.P. and Cowsert,L.M.
  TITLE     Antisense inhibition of hepatitis B virus replication
  JOURNAL   Patent: US 5985662-A 7 16-NOV-1999;
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Db          3 AAAGCCACCCAAGGCA 18


RESULT 15
I55196
LOCUS       I55196                    21 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 45 from patent US 5646262.
ACCESSION   I55196
VERSION     I55196.1  GI:2476399
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Korba,B.E. and Gerin,J.L.
  TITLE     Antisense oligonucleotides against hepatitis B viral replication
  JOURNAL   Patent: US 5646262-A 45 08-JUL-1997;
FEATURES             Location/Qualifiers
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Job time : 1454 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 29, 2005, 03:23:25 ; Search time 272 Seconds
(without alignments)
348.220 Million cell updates/sec

Title: US-09-888-164-29
Perfect score: 16
Sequence: 1 aaagccacccaaggca 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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c	5	16	100.0	17	8	ACD53930	Acd53930 HBV zinzy
c	6	16	100.0	17	12	ADM59621	Adm59621 Hepatitis
c	7	16	100.0	17	12	ADM60244	Adm60244 Hepatitis
	8	16	100.0	18	2	AAT71786	Aat71786 Hepatitis
	9	16	100.0	18	2	AAV14133	Aav14133 Probe HBP
c	10	16	100.0	19	2	AAT71785	Aat71785 Hepatitis
c	11	16	100.0	19	2	AAT71789	Aat71789 Hepatitis
c	12	16	100.0	19	11	ADM00160	Adm00160 Hepatitis
	13	16	100.0	19	11	ADM00806	Adm00806 Hepatitis
	14	16	100.0	19	11	ADM00807	Adm00807 Hepatitis
	15	16	100.0	19	11	ADM00284	Adm00284 Hepatitis
	16	16	100.0	19	11	ADM00804	Adm00804 Hepatitis
c	17	16	100.0	19	11	ADL99637	Adl99637 Hepatitis
c	18	16	100.0	19	11	ADM00161	Adm00161 Hepatitis
c	19	16	100.0	19	11	ADM00158	Adm00158 Hepatitis
c	20	16	100.0	20	2	AAQ13771	Aaq13771 HBV prime
c	21	16	100.0	20	2	AAQ13772	Aaq13772 HBV prime
	22	16	100.0	20	2	AAQ85970	Aaq85970 Hepatitis
	23	16	100.0	20	2	AAT70947	Aat70947 HBV pre-g
	24	16	100.0	21	2	AAQ92909	Aaq92909 Antiviral
	25	16	100.0	21	2	AAT18255	Aat18255 HBV epsil
	26	16	100.0	21	2	AAT18253	Aat18253 HBV epsil
	27	16	100.0	21	2	AAT70936	Aat70936 HBV core
c	28	16	100.0	21	9	ADA13842	Ada13842 Short int
c	29	16	100.0	21	11	ADM00924	Adm00924 Hepatitis
c	30	16	100.0	23	2	AAQ13770	Aaq13770 HBV prime
c	31	16	100.0	23	2	AAT03266	Aat03266 Hepatitis
c	32	16	100.0	23	2	AAQ81424	Aaq81424 HBV hybri
c	33	16	100.0	23	4	AAD19005	Aad19005 Hepatitis
c	34	16	100.0	23	11	ADM00880	Adm00880 Hepatitis
c	35	16	100.0	30	2	AAV29303	Aav29303 Hepatitis
c	36	16	100.0	32	4	AAS14628	Aas14628 NASBA mol
c	37	16	100.0	44	2	AAT71784	Aat71784 Hepatitis
c	38	16	100.0	44	2	AAT71783	Aat71783 Hepatitis
c	39	16	100.0	48	3	ABK14698	Abk14698 HBV encap
c	40	16	100.0	48	3	ABK14696	Abk14696 RNA targe
c	41	16	100.0	50	2	AAQ81436	Aaq81436 HBV targe
c	42	16	100.0	54	3	AAZ94421	Aaz94421 Hepatitis
c	43	16	100.0	61	3	ABK14697	Abk14697 HBV prege
c	44	16	100.0	61	9	ACA62424	Aca62424 Hepatitis
c	45	16	100.0	70	2	AAQ28267	Aaq28267 Sequence

ALIGNMENTS

RESULT 1
AAT18256
ID AAT18256 standard; DNA; 16 BP.
XX
AC AAT18256;
XX
DT 17-SEP-1996 (first entry)
XX
DE HBV epsilon encapsidation mRNA intermediate antisense oligo L2c.
XX
KW Inhibition; replication; hepatitis B virus; HBV; antisense; mRNA;
KW epsilon; encapsidation; sequence; intermediate; subtype ayw; C gene;
KW treatment; chronic infection; modulation; translation; transcription;
KW release; host cell; ss.
XX
OS Synthetic.
XX
PN WO9603152-A1.
XX
PD 08-FEB-1996.
XX
PF 28-JUL-1995; 95WO-US009143.
XX
PR 28-JUL-1994; 94US-00281106.
XX
PA (GEOU) UNIV GEORGETOWN.
XX
PI Korba BE, Gerin JL;
XX
DR WPI; 1996-116796/12.
XX
PT Single stranded oligo:nucleotide(s) for inhibiting replication of
PT hepatitis B virus - are anti-sense to portions of the epsilon
PT encapsidation sequence and modulate HBV function.
XX
PS Claim 15; Page 44; 56pp; English.
XX
CC The present sequence, which inhibits the replication of hepatitis B virus
CC (HBV) in a host cell, is a single stranded antisense oligonucleotide that
CC binds the epsilon encapsidation sequence of a mRNA intermediate derived
CC from the HBV genome. The 1st nucleotide of the oligonucleotide
CC corresponds to nucleotide 1884 of the HBV ayw subtype C gene, using the
CC numbering scheme from the sequence published by Galibert et al., Nature

```
CC   281: 646 (1979). A compsn. comprising the oligonucleotide may be used to
CC   treat chronic HBV infection by modulating a HBV related function, e.g.
CC   translation, transcription, encapsidation, replication and release from a
CC   host cell. The effect of the oligonucleotide on the levels of HBV DNA in
CC   the extracellular medium (VIR. DNA), intracellular viral replicative
CC   intermediates (HBV RI), intracellular viral RNA (HBV RNA), HBV surface
CC   antigen protein (HBsAg), HBV e antigen protein (HBeAg) and HBV core
CC   antigen protein (HBcAg), given as the EC(90) (microM, 9 days of
CC   treatment) or ND (not determined), are VIR. DNA (1.6), HBV RI (5.1), HBV
CC   RNA (>20), HBsAg (>20), HBeAg (>20) and HBcAg (18.5)
XX
SQ   Sequence 16 BP; 7 A; 6 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 16;  DB 2;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 2
AAV14125
ID   AAV14125 standard; DNA; 16 BP.
XX
AC   AAV14125;
XX
DT   27-AUG-2003  (revised)
DT   19-MAY-1998  (first entry)
XX
DE   Probe HBPr41 for preCore region of HBV.
XX
KW   Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis;
KW   preCore region; HBsAg region; genotype specific target;
KW   mutation detection; ss.
XX
OS   Synthetic.
OS   Hepatitis B virus.
XX
PN   WO9740193-A2.
XX
PD   30-OCT-1997.
XX
PF   21-APR-1997;   97WO-EP002002.
XX
PR   19-APR-1996;   96EP-00870053.
XX
PA   (INNO-) INNOGENETICS NV.
XX
PI   Stuyver L,  Rossau R,  Maertens G;
XX
DR   WPI; 1997-535867/49.
XX
PT   Detection and/or genetic analysis of hepatitis B virus - specifically
PT   genotype, preCore mutations, vaccine escape mutations and RT gene
PT   mutations selected by treatment with drugs.
XX
PS   Claim 5; Page 27; 80pp; English.
XX
CC   This sequence represents a probe for the preCore region of hepatitis b
CC   virus (HBV). This sequence can be used in the method of the invention for
CC   detection and/or genetic analysis of hepatitis B virus (HBV) in a sample.
CC   The method comprises: (a) optionally releasing, isolating or
CC   concentrating polynucleic acids (I) in the sample, and amplifying the
CC   relevant part of a suitable HBV gene in the sample with at least 1
CC   suitable primer pair; (b) hybridising (I) with a combination of at least
CC   2 nucleotide probes, which are applied to known locations on a solid
CC   support and hybridise specifically to mutant target sequences chosen from
CC   the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
CC   genotype specific target sequences, or their complements or U for T
CC   homologues; (c) detecting the hybrids formed in step (b), and inferring
CC   the HBV genotype and/or mutants present in the sample from the
CC   differential hybridisation signal(s). The composition can be used to
CC   diagnose and/or monitor HBV mutants and/or genotypes in a sample,
CC   specifically genotype, preCore mutations, vaccine escape mutations and RT
CC   gene mutations selected by treatment with drugs, e.g. lamivudune and
CC   penciclovir. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ   Sequence 16 BP; 7 A; 6 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 16;  DB 2;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 3
ADB68575
ID   ADB68575 standard; DNA; 16 BP.
XX
AC   ADB68575;
XX
DT   04-DEC-2003  (first entry)
XX
DE   NG3 A-L-P conjugate DNA component used to target HBV e-site.
XX
KW   homogeneous A-L-P conjugate; hepatic; chronic viral hepatitis; cirrhosis;
KW   malaria; viral infection; protozoan; cancer; hepatocellular carcinoma;
KW   HCC; ss; NG3; HBV; e-site; pregenome.
XX
OS   Hepatitis B virus.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .16
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER = phosphorothioate backbone"
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER = Optionally linked to YEE(ahGalNAc)3-SMCC
FT                   and various chemical groups as shown in figures"
FT   modified_base   16
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "OTHER = Optionally linked to chemical group as
FT                   shown in figure 5"
XX
PN   WO2003067209-A2.
XX
PD   14-AUG-2003.
XX
PF   21-JUN-2002; 2002WO-US019908.
XX
PR   22-JUN-2001; 2001US-00888164.
XX
PA   (CELL-) CELL WORKS INC.
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Ts'o POP,  Duff R,  Zhou Y,  Deamond S,  Roby C;
XX
DR   WPI; 2003-697456/66.
XX
PT   New homogeneous prodrug conjugate containing hepatic ligand for delivery
PT   of pathogen-specific oligomer useful for treating liver infections or
PT   cancer.
XX
PS   Claim 7; Page 83; 107pp; English.
XX
CC   The invention relates to a novel homogeneous conjugate comprising a
CC   hepatic ligand, bifunctional linker and biologically stable oligomer that
CC   binds to a sequence in a hepatic virus or pathogen and is released from
```

```
CC   the conjugate by hydrolysis or reduction. The conjugate of the invention
CC   may be useful during the treatment of liver diseases including chronic
CC   viral hepatitis, cirrhosis, malaria, viral or protozoan infection and
CC   cancer, such as hepatocellular carcinoma (HCC). The current sequence is
CC   that of the NG3 A-L-P conjugate DNA component of the invention which was
CC   used to target the Hepatitis B virus (HBV) pregenome (e-site).
XX
SQ   Sequence 16 BP; 7 A; 6 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 16;  DB 10;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 4
ACD55710/c
ID   ACD55710 standard; RNA; 17 BP.
XX
AC   ACD55710;
XX
DT   23-SEP-2003  (first entry)
XX
DE   HBV amberzyme substrate sequence #183.
XX
KW   Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW   RNA stability; RNA expression; RNA synthesis; antisense;
KW   enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW   amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW   HBV reverse transcriptase; Enhancer I region; viral replication;
KW   degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW   liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW   virucide; antiinflammatory; substrate; ss.
XX
OS   Hepatitis B virus.
XX
PN   WO200281494-A1.
XX
PD   17-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009187.
XX
PR   26-MAR-2001; 2001US-00817879.
PR   08-JUN-2001; 2001US-00877478.
PR   08-JUN-2001; 2001US-0296876P.
PR   24-OCT-2001; 2001US-0335059P.
PR   05-DEC-2001; 2001US-0337055P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MACE/) MACEJAK D.
PA   (MCSW/) MCSWIGGEN J.
PA   (MORR/) MORRISSEY D.
PA   (PAVC/) PAVCO P.
PA   (LEEP/) LEE P.
PA   (DRAP/) DRAPER K.
PA   (ROBE/) ROBERTS E.
XX
PI   Blatt L,  Macejak D,  Mcswiggen J,  Morrissey D,  Pavco P,  Lee P;
PI   Draper K,  Roberts E;
XX
DR   WPI; 2003-229207/22.
XX
PT   Novel compound useful for treating cirrhosis, liver failure,
PT   hepatocellular carcinoma, or condition associated with hepatitis C virus
PT   infection.
XX
PS   Example 1; Page 207; 387pp; English.
XX
CC   The present invention relates to nucleic acid molecules which modulate
CC   the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC   Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC   and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
CC   inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC   are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC   transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC   as oligonucleotides that specifically bind the Enhancer I region of HBV
CC   DNA. The nucleic acids may be used to modulate the expression of HBV
CC   genes and HBV viral replication. Also disclosed is a method for screening
CC   compounds and/or potential therapies directed against HBV, and compounds
CC   that modulate the expression and/or replication of HCV. The compounds and
CC   methods of the invention are useful for the treatment of degenerative and
CC   disease states related to HBV and HCV infection, replication and gene
CC   expression such as cirrhosis, liver failure, and hepatocellular
CC   carcinoma. The present sequence represents a substrate for one of the HBV
CC   ribozyme, inozyme, G-cleaver, zinzyme, DNAzyme or amberzyme sequences
CC   disclosed in the present invention
XX
SQ   Sequence 17 BP; 0 A; 3 C; 7 G; 0 T; 7 U; 0 Other;

  Query Match             100.0%;  Score 16;  DB 8;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         17 AAAGCCACCCAAGGCA 2


RESULT 5
ACD53930/c
ID   ACD53930 standard; RNA; 17 BP.
XX
AC   ACD53930;
XX
DT   24-SEP-2003  (first entry)
XX
DE   HBV zinzyme substrate sequence #100.
XX
KW   Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW   RNA stability; RNA expression; RNA synthesis; antisense;
KW   enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW   amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW   HBV reverse transcriptase; Enhancer I region; viral replication;
KW   degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW   liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW   virucide; antiinflammatory; substrate; ss.
XX
OS   Hepatitis B virus.
XX
PN   WO200281494-A1.
XX
PD   17-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009187.
XX
PR   26-MAR-2001; 2001US-00817879.
PR   08-JUN-2001; 2001US-00877478.
PR   08-JUN-2001; 2001US-0296876P.
PR   24-OCT-2001; 2001US-0335059P.
PR   05-DEC-2001; 2001US-0337055P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MACE/) MACEJAK D.
PA   (MCSW/) MCSWIGGEN J.
PA   (MORR/) MORRISSEY D.
PA   (PAVC/) PAVCO P.
PA   (LEEP/) LEE P.
PA   (DRAP/) DRAPER K.
PA   (ROBE/) ROBERTS E.
XX
PI   Blatt L,  Macejak D,  Mcswiggen J,  Morrissey D,  Pavco P,  Lee P;
```

PI Draper K, Roberts E;
XX
DR WPI; 2003-229207/22.
XX
PT Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
PS Example 1; Page 175; 387pp; English.
XX
CC The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HBV
CC ribozyme, inozyme, G-cleaver, zinzyme, DNAzyme or amberzyme sequences
CC disclosed in the present invention
XX
SQ Sequence 17 BP; 0 A; 3 C; 7 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 16; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAAGGCA 16
||||||||||||||||
Db 16 AAAGCCACCCAAGGCA 1

RESULT 6
ADM59621/c
ID ADM59621 standard; RNA; 17 BP.
XX
AC ADM59621;
XX
DT 03-JUN-2004 (first entry)
XX
DE Hepatitis B virus (HBV) RNA target sequence #1755.
XX
KW Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;
KW hepatitis B virus infection; hepatitis; hepatocellular carcinoma;
KW cirrhosis; liver failure; lamivudine; interferon; genetic drift;
KW virucide; hepatotropic; antiinflammatory; cytostatic.
XX
OS Hepatitis B virus.
XX
PN US2004054156-A1.
XX
PD 18-MAR-2004.
XX
PF 15-JAN-2003; 2003US-00342902.
XX
PR 14-MAY-1992; 92US-00882712.
PR 07-FEB-1994; 94US-00193627.
PR 08-NOV-1999; 99US-00436430.
PR 20-MAR-2000; 2000US-00531025.
PR 09-AUG-2000; 2000US-00636385.
PR 24-OCT-2000; 2000US-00696347.
PR 08-JUN-2001; 2001US-00877478.
XX
PA (DRAP/) DRAPER K.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (MORR/) MORRISSEY D.
XX
PI Draper K, Blatt L, Mcswiggen JA, Morrissey D;
XX
DR WPI; 2004-247781/23.
XX
PT Novel enzymatic nucleic acid molecule such as DNAzymes and inozymes
PT specifically cleaving RNA derived from hepatitis B virus and comprising
PT one or more binding arms, useful for treating hepatitis and cirrhosis.
XX
PS Disclosure; SEQ ID NO 1755; 122pp; English.
XX
CC The invention relates to an enzymatic nucleic acid molecule that
CC specifically cleaves RNA derived from hepatitis B virus (HBV) and
CC comprising one or more binding arms, without requiring the presence of a
CC 2'-OH group within the molecule for activity. The nucleic acids are
CC useful for treating hepatitis B virus infection, hepatitis,
CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in
CC combination with other therapies such as lamivudine and interferons. The
CC nucleic acids are useful as diagnostic tools to examine genetic drift and
CC mutations within diseased cells, for detecting the presence of HBV RNA in
CC a cell, for the study of RNA and for down-regulating gene expression of
CC target genes in bacterial, fungal, viral, plant or mammalian cells. This
CC sequence represents an HBV RNA target sequence, used in the scope of the
CC invention. Note: The sequence data for this patent is also available in
CC electronic format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 17 BP; 0 A; 3 C; 7 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 16; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAAGGCA 16
||||||||||||||||
Db 16 AAAGCCACCCAAGGCA 1

RESULT 7
ADM60244/c
ID ADM60244 standard; RNA; 17 BP.
XX
AC ADM60244;
XX
DT 03-JUN-2004 (first entry)
XX
DE Hepatitis B virus (HBV) RNA target sequence #2378.
XX
KW Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;
KW hepatitis B virus infection; hepatitis; hepatocellular carcinoma;
KW cirrhosis; liver failure; lamivudine; interferon; genetic drift;
KW virucide; hepatotropic; antiinflammatory; cytostatic.
XX
OS Hepatitis B virus.
XX
PN US2004054156-A1.
XX
PD 18-MAR-2004.
XX
PF 15-JAN-2003; 2003US-00342902.
XX
PR 14-MAY-1992; 92US-00882712.
PR 07-FEB-1994; 94US-00193627.
PR 08-NOV-1999; 99US-00436430.
PR 20-MAR-2000; 2000US-00531025.
PR 09-AUG-2000; 2000US-00636385.
PR 24-OCT-2000; 2000US-00696347.
PR 08-JUN-2001; 2001US-00877478.
XX
PA (DRAP/) DRAPER K.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.

PA (MORR/) MORRISSEY D.
XX
PI Draper K, Blatt L, Mcswiggen JA, Morrissey D;
XX
DR WPI; 2004-247781/23.
XX
PT Novel enzymatic nucleic acid molecule such as DNAzymes and inozymes
PT specifically cleaving RNA derived from hepatitis B virus and comprising
PT one or more binding arms, useful for treating hepatitis and cirrhosis.
XX
PS Disclosure; SEQ ID NO 2378; 122pp; English.
XX
CC The invention relates to an enzymatic nucleic acid molecule that
CC specifically cleaves RNA derived from hepatitis B virus (HBV) and
CC comprising one or more binding arms, without requiring the presence of a
CC 2'-OH group within the molecule for activity. The nucleic acids are
CC useful for treating hepatitis B virus infection, hepatitis,
CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in
CC combination with other therapies such as lamivudine and interferons. The
CC nucleic acids are useful as diagnostic tools to examine genetic drift and
CC mutations within diseased cells, for detecting the presence of HBV RNA in
CC a cell, for the study of RNA and for down-regulating gene expression of
CC target genes in bacterial, fungal, viral, plant or mammalian cells. This
CC sequence represents an HBV RNA target sequence, used in the scope of the
CC invention. Note: The sequence data for this patent is also available in
CC electronic format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 17 BP; 0 A; 3 C; 7 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 16; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAAGGCA 16
||||||||||||||||
Db 17 AAAGCCACCCAAGGCA 2

RESULT 8
AAT71786
ID AAT71786 standard; DNA; 18 BP.
XX
AC AAT71786;
XX
DT 29-AUG-1997 (first entry)
XX
DE Hepatitis B virus precore antigen wild-type target sequence primer.
XX
KW HBV; ligase chain reaction; internal standard; amplification; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1
FT /*tag= a
FT /note= "Phosphorylated"
FT misc_difference 18
FT /*tag= b
FT /note= "Haptenated with fluoroscein"
XX
PN WO9640996-A1.
XX
PD 19-DEC-1996.
XX
PF 03-JUN-1996; 96WO-US008429.
XX
PR 07-JUN-1995; 95US-00480220.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Birkenmeyer L, Mushahwar IK;
XX
DR WPI; 1997-052367/05.
XX
PT Quantitative detection of target nucleic acid sequence, esp. hepatitis B
PT virus - can distinguish wild-type and mutant DNA types.
XX
PS Claim 14; Page 29; 40pp; English.
XX
CC A novel method has been produced for detecting the amount of a target
CC nucleic acid sequence which may be present in a test sample. It involves
CC contacting the test sample with means for performing a nucleic acid
CC amplification reaction; and determining the ratio of target amplification
CC products to internal standard amplification products present in the
CC sample. The present sequence represents a primer/target specific probe
CC for the hepatitis B virus (HBV) precore antigen wild-type target sequence
CC (AAT71783). The method can be used for distinguishing between two
CC different nucleic acid sequences present in a sample e.g. wild-type and
CC mutant. The compositions can be used for quantitatively detecting the DNA
CC of HBV
XX
SQ Sequence 18 BP; 8 A; 7 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAAGGCA 16
||||||||||||||||
Db 1 AAAGCCACCCAAGGCA 16

RESULT 9
AAV14133
ID AAV14133 standard; DNA; 18 BP.
XX
AC AAV14133;
XX
DT 27-AUG-2003 (revised)
DT 19-MAY-1998 (first entry)
XX
DE Probe HBPr49 for preCore region of HBV.
XX
KW Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis;
KW preCore region; HBsAg region; genotype specific target;
KW mutation detection; ss.
XX
OS Synthetic.
OS Hepatitis B virus.
XX
PN WO9740193-A2.
XX
PD 30-OCT-1997.
XX
PF 21-APR-1997; 97WO-EP002002.
XX
PR 19-APR-1996; 96EP-00870053.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Stuyver L, Rossau R, Maertens G;
XX
DR WPI; 1997-535867/49.
XX
PT Detection and/or genetic analysis of hepatitis B virus - specifically
PT genotype, preCore mutations, vaccine escape mutations and RT gene
PT mutations selected by treatment with drugs.
XX
PS Claim 5; Page 27; 80pp; English.
XX
CC This sequence represents a probe for the preCore region of hepatitis b
CC virus (HBV). This sequence can be used in the method of the invention for
CC detection and/or genetic analysis of hepatitis B virus (HBV) in a sample.
CC The method comprises: (a) optionally releasing, isolating or
CC concentrating polynucleic acids (I) in the sample, and amplifying the
CC relevant part of a suitable HBV gene in the sample with at least 1

```
CC   suitable primer pair; (b) hybridising (I) with a combination of at least
CC   2 nucleotide probes, which are applied to known locations on a solid
CC   support and hybridise specifically to mutant target sequences chosen from
CC   the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
CC   genotype specific target sequences, or their complements or U for T
CC   homologues; (c) detecting the hybrids formed in step (b), and inferring
CC   the HBV genotype and/or mutants present in the sample from the
CC   differential hybridisation signal(s). The composition can be used to
CC   diagnose and/or monitor HBV mutants and/or genotypes in a sample,
CC   specifically genotype, preCore mutations, vaccine escape mutations and RT
CC   gene mutations selected by treatment with drugs, e.g. lamivudune and
CC   penciclovir. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ   Sequence 18 BP; 8 A; 7 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 16;  DB 2;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
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Db          1 AAAGCCACCCAAGGCA 16


RESULT 10
AAT71785/c
ID   AAT71785 standard; DNA; 19 BP.
XX
AC   AAT71785;
XX
DT   29-AUG-1997  (first entry)
XX
DE   Hepatitis B virus precore antigen wild-type target sequence primer.
XX
KW   HBV; ligase chain reaction; internal standard; amplification; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1
FT                   /*tag=  a
FT                   /note= "Haptenated with fluoroscein"
XX
PN   WO9640996-A1.
XX
PD   19-DEC-1996.
XX
PF   03-JUN-1996;   96WO-US008429.
XX
PR   07-JUN-1995;   95US-00480220.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Birkenmeyer L,  Mushahwar IK;
XX
DR   WPI; 1997-052367/05.
XX
PT   Quantitative detection of target nucleic acid sequence, esp. hepatitis B
PT   virus - can distinguish wild-type and mutant DNA types.
XX
PS   Claim 14; Page 29; 40pp; English.
XX
CC   A novel method has been produced for detecting the amount of a target
CC   nucleic acid sequence which may be present in a test sample. It involves
CC   contacting the test sample with means for performing a nucleic acid
CC   amplification reaction; and determining the ratio of target amplification
CC   products to internal standard amplification products present in the
CC   sample. The present sequence represents a primer/target specific probe
CC   for the hepatitis B virus (HBV) precore antigen wild-type target sequence
CC   (AAT71783). The method can be used for distinguishing between two
CC   different nucleic acid sequences present in a sample e.g. wild-type and
CC   mutant. The compositions can be used for quantitatively detecting the DNA
CC   of HBV
XX
SQ   Sequence 19 BP; 0 A; 3 C; 8 G; 8 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 16;  DB 2;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         18 AAAGCCACCCAAGGCA 3


RESULT 11
AAT71789/c
ID   AAT71789 standard; DNA; 19 BP.
XX
AC   AAT71789;
XX
DT   29-AUG-1997  (first entry)
XX
DE   Hepatitis B virus precore antigen mutant target sequence primer.
XX
KW   HBV; ligase chain reaction; internal standard; amplification; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1
FT                   /*tag=  a
FT                   /note= "Haptenated with fluorescein"
XX
PN   WO9640996-A1.
XX
PD   19-DEC-1996.
XX
PF   03-JUN-1996;   96WO-US008429.
XX
PR   07-JUN-1995;   95US-00480220.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Birkenmeyer L,  Mushahwar IK;
XX
DR   WPI; 1997-052367/05.
XX
PT   Quantitative detection of target nucleic acid sequence, esp. hepatitis B
PT   virus - can distinguish wild-type and mutant DNA types.
XX
PS   Claim 14; Page 30; 40pp; English.
XX
CC   A novel method has been produced for detecting the amount of a target
CC   nucleic acid sequence which may be present in a test sample. It involves
CC   contacting the test sample with means for performing a nucleic acid
CC   amplification reaction; and determining the ratio of target amplification
CC   products to internal standard amplification products present in the
CC   sample. The present sequence represents a primer/target specific probe
CC   for the hepatitis B virus (HBV) precore antigen mutant target sequence
CC   (AAT71784). The method can be used for distinguishing between two
CC   different nucleic acid sequences present in a sample e.g. wild-type and
CC   mutant. The compositions can be used for quantitatively detecting the DNA
CC   of HBV
XX
SQ   Sequence 19 BP; 1 A; 3 C; 7 G; 8 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 16;  DB 2;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         18 AAAGCCACCCAAGGCA 3
```

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RESULT 12
ADM00160/c
ID   ADM00160 standard; RNA; 19 BP.
XX
AC   ADM00160;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Hepatitis B virus short interfering nucleic acid (siNA) #576.
XX
KW   Virucide; Hepatotropic; Gene therapy; ss; short interfering nucleic acid;
KW   siNA; hepatitis B virus; HBV; RNA interference.
XX
OS   Hepatitis B virus.
XX
PN   US2003206887-A1.
XX
PD   06-NOV-2003.
XX
PF   16-SEP-2002; 2002US-00244647.
XX
PR   14-MAY-1992;   92US-00882712.
PR   07-FEB-1994;   94US-00193627.
PR   08-NOV-1999;   99US-00436430.
PR   20-MAR-2000; 2000US-00531025.
PR   09-AUG-2000; 2000US-00636385.
PR   24-OCT-2000; 2000US-00696347.
PR   08-JUN-2001; 2001US-00877478.
PR   08-JUN-2001; 2001US-0296876P.
PR   24-OCT-2001; 2001US-0335059P.
PR   05-DEC-2001; 2001US-0337055P.
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   26-MAR-2002; 2002WO-US009187.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
XX
PA   (MORR/) MORRISSEY D.
PA   (MCSW/) MCSWIGGEN J A.
PA   (BEIG/) BEIGELMAN L.
XX
PI   Morrissey D,  Mcswiggen JA,  Beigelman L;
XX
DR   WPI; 2003-901032/82.
XX
PT   New short interfering nucleic acid molecules which down-regulates
PT   expression of a hepatitis B virus (HBV) or which inhibits HBV
PT   replication, useful for treating human HBV infections or for
PT   characterizing gene function.
XX
PS   Claim 11; Page 48; 72pp; English.
XX
CC   The invention relates to a short interfering nucleic acid (siNA) molecule
CC   that down-regulates expression of a hepatitis B virus (HBV) gene by RNA
CC   interference or that inhibits HBV replication. Also disclosed are the
CC   following: (i) a method of modulating the expression of a HBV gene in a
CC   tissue explant; (ii)) a method of generating a library of siNA constructs
CC   having predetermined complexity; (iii) a cell containing one or more siNA
CC   molecules; (iv)a kit containing a siNA molecule which can be used to
CC   modulate the expression of a HBV target gene in a cell, tissue or
CC   organism; and (v) a method for synthesising a siNA molecule. The siNA
CC   molecule is adapted for use to treat HBV infection, and comprises a sense
CC   and an antisense region, where the antisense region comprises sequence
CC   complementary to an RNA sequence encoding HBV and the sense region
CC   comprises sequence complementary to the antisense region. The siNA
CC   molecule is assembled from 2 nucleic acid fragments, where one fragment
CC   comprises the sense region and the second fragment comprises the
CC   antisense region of the siNA molecule, where sense region and the
CC   antisense region comprise separate oligonucleotides, and are covalently
CC   connected via a linker molecule. The linker molecule is a polynucleotide
CC   linker or a non-nucleotide linker. The sense region comprises a 3'-
CC   terminal overhang and the antisense region comprises a 3'-terminal
CC   overhang. The 3'-terminal overhangs each comprise about 2 nucleotides.
CC   The antisense region 3'-terminal overhang is complementary to RNA
CC   encoding HBV. The siNA is useful for treating human hepatitis B virus
CC   infections, and for characterising pathways of gene function, e.g. to
CC   inhibit activity of target genes in a pathway to determine the function
CC   of uncharacterised genes in gene function analysis. The siNA molecules
CC   may also be used in clinical, industrial, environmental, agricultural
CC   and/or research settings. The present sequence represents 1 of 1504 HBV
CC   siNA molecules of the invention.
XX
SQ   Sequence 19 BP; 0 A; 3 C; 9 G; 0 T; 7 U; 0 Other;

  Query Match             100.0%;  Score 16;  DB 11;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              ||||||||||||||||
Db         16 AAAGCCACCCAAGGCA 1


RESULT 13
ADM00806
ID   ADM00806 standard; RNA; 19 BP.
XX
AC   ADM00806;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Hepatitis B virus short interfering nucleic acid (siNA) #1222.
XX
KW   Virucide; Hepatotropic; Gene therapy; ss; short interfering nucleic acid;
KW   siNA; hepatitis B virus; HBV; RNA interference.
XX
OS   Hepatitis B virus.
XX
PN   US2003206887-A1.
XX
PD   06-NOV-2003.
XX
PF   16-SEP-2002; 2002US-00244647.
XX
PR   14-MAY-1992;   92US-00882712.
PR   07-FEB-1994;   94US-00193627.
PR   08-NOV-1999;   99US-00436430.
PR   20-MAR-2000; 2000US-00531025.
PR   09-AUG-2000; 2000US-00636385.
PR   24-OCT-2000; 2000US-00696347.
PR   08-JUN-2001; 2001US-00877478.
PR   08-JUN-2001; 2001US-0296876P.
PR   24-OCT-2001; 2001US-0335059P.
PR   05-DEC-2001; 2001US-0337055P.
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   26-MAR-2002; 2002WO-US009187.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
XX
PA   (MORR/) MORRISSEY D.
PA   (MCSW/) MCSWIGGEN J A.
PA   (BEIG/) BEIGELMAN L.
XX
PI   Morrissey D,  Mcswiggen JA,  Beigelman L;
XX
DR   WPI; 2003-901032/82.
XX
PT   New short interfering nucleic acid molecules which down-regulates
PT   expression of a hepatitis B virus (HBV) or which inhibits HBV
PT   replication, useful for treating human HBV infections or for
PT   characterizing gene function.
```

```
XX
PS   Claim 11; Page 48; 72pp; English.
XX
CC   The invention relates to a short interfering nucleic acid (siNA) molecule
CC   that down-regulates expression of a hepatitis B virus (HBV) gene by RNA
CC   interference or that inhibits HBV replication. Also disclosed are the
CC   following: (i) a method of modulating the expression of a HBV gene in a
CC   tissue explant; (ii)) a method of generating a library of siNA constructs
CC   having predetermined complexity; (iii) a cell containing one or more siNA
CC   molecules; (iv)a kit containing a siNA molecule which can be used to
CC   modulate the expression of a HBV target gene in a cell, tissue or
CC   organism; and (v) a method for synthesising a siNA molecule. The siNA
CC   molecule is adapted for use to treat HBV infection, and comprises a sense
CC   and an antisense region, where the antisense region comprises sequence
CC   complementary to an RNA sequence encoding HBV and the sense region
CC   comprises sequence complementary to the antisense region. The siNA
CC   molecule is assembled from 2 nucleic acid fragments, where one fragment
CC   comprises the sense region and the second fragment comprises the
CC   antisense region of the siNA molecule, where sense region and the
CC   antisense region comprise separate oligonucleotides, and are covalently
CC   connected via a linker molecule. The linker molecule is a polynucleotide
CC   linker or a non-nucleotide linker. The sense region comprises a 3'-
CC   terminal overhang and the antisense region comprises a 3'-terminal
CC   overhang. The 3'-terminal overhangs each comprise about 2 nucleotides.
CC   The antisense region 3'-terminal overhang is complementary to RNA
CC   encoding HBV. The siNA is useful for treating human hepatitis B virus
CC   infections, and for characterising pathways of gene function, e.g. to
CC   inhibit activity of target genes in a pathway to determine the function
CC   of uncharacterised genes in gene function analysis. The siNA molecules
CC   may also be used in clinical, industrial, environmental, agricultural
CC   and/or research settings. The present sequence represents 1 of 1504 HBV
CC   siNA molecules of the invention.
XX
SQ   Sequence 19 BP; 7 A; 9 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 16;  DB 11;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          4 AAAGCCACCCAAGGCA 19


RESULT 14
ADM00807
ID   ADM00807 standard; RNA; 19 BP.
XX
AC   ADM00807;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Hepatitis B virus short interfering nucleic acid (siNA) #1223.
XX
KW   Virucide; Hepatotropic; Gene therapy; ss; short interfering nucleic acid;
KW   siNA; hepatitis B virus; HBV; RNA interference.
XX
OS   Hepatitis B virus.
XX
PN   US2003206887-A1.
XX
PD   06-NOV-2003.
XX
PF   16-SEP-2002; 2002US-00244647.
XX
PR   14-MAY-1992;   92US-00882712.
PR   07-FEB-1994;   94US-00193627.
PR   08-NOV-1999;   99US-00436430.
PR   20-MAR-2000; 2000US-00531025.
PR   09-AUG-2000; 2000US-00636385.
PR   24-OCT-2000; 2000US-00696347.
PR   08-JUN-2001; 2001US-00877478.
PR   08-JUN-2001; 2001US-0296876P.
PR   24-OCT-2001; 2001US-0335059P.
PR   05-DEC-2001; 2001US-0337055P.
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   26-MAR-2002; 2002WO-US009187.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
XX
PA   (MORR/) MORRISSEY D.
PA   (MCSW/) MCSWIGGEN J A.
PA   (BEIG/) BEIGELMAN L.
XX
PI   Morrissey D,  Mcswiggen JA,  Beigelman L;
XX
DR   WPI; 2003-901032/82.
XX
PT   New short interfering nucleic acid molecules which down-regulates
PT   expression of a hepatitis B virus (HBV) or which inhibits HBV
PT   replication, useful for treating human HBV infections or for
PT   characterizing gene function.
XX
PS   Claim 11; Page 48; 72pp; English.
XX
CC   The invention relates to a short interfering nucleic acid (siNA) molecule
CC   that down-regulates expression of a hepatitis B virus (HBV) gene by RNA
CC   interference or that inhibits HBV replication. Also disclosed are the
CC   following: (i) a method of modulating the expression of a HBV gene in a
CC   tissue explant; (ii)) a method of generating a library of siNA constructs
CC   having predetermined complexity; (iii) a cell containing one or more siNA
CC   molecules; (iv)a kit containing a siNA molecule which can be used to
CC   modulate the expression of a HBV target gene in a cell, tissue or
CC   organism; and (v) a method for synthesising a siNA molecule. The siNA
CC   molecule is adapted for use to treat HBV infection, and comprises a sense
CC   and an antisense region, where the antisense region comprises sequence
CC   complementary to an RNA sequence encoding HBV and the sense region
CC   comprises sequence complementary to the antisense region. The siNA
CC   molecule is assembled from 2 nucleic acid fragments, where one fragment
CC   comprises the sense region and the second fragment comprises the
CC   antisense region of the siNA molecule, where sense region and the
CC   antisense region comprise separate oligonucleotides, and are covalently
CC   connected via a linker molecule. The linker molecule is a polynucleotide
CC   linker or a non-nucleotide linker. The sense region comprises a 3'-
CC   terminal overhang and the antisense region comprises a 3'-terminal
CC   overhang. The 3'-terminal overhangs each comprise about 2 nucleotides.
CC   The antisense region 3'-terminal overhang is complementary to RNA
CC   encoding HBV. The siNA is useful for treating human hepatitis B virus
CC   infections, and for characterising pathways of gene function, e.g. to
CC   inhibit activity of target genes in a pathway to determine the function
CC   of uncharacterised genes in gene function analysis. The siNA molecules
CC   may also be used in clinical, industrial, environmental, agricultural
CC   and/or research settings. The present sequence represents 1 of 1504 HBV
CC   siNA molecules of the invention.
XX
SQ   Sequence 19 BP; 8 A; 8 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 16;  DB 11;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          2 AAAGCCACCCAAGGCA 17


RESULT 15
ADM00284
ID   ADM00284 standard; RNA; 19 BP.
XX
AC   ADM00284;
XX
DT   20-MAY-2004  (first entry)
```

XX
DE Hepatitis B virus short interfering nucleic acid (siNA) #700.
XX
KW Virucide; Hepatotropic; Gene therapy; ss; short interfering nucleic acid;
KW siNA; hepatitis B virus; HBV; RNA interference.
XX
OS Hepatitis B virus.
XX
PN US2003206887-A1.
XX
PD 06-NOV-2003.
XX
PF 16-SEP-2002; 2002US-00244647.
XX
PR 14-MAY-1992; 92US-00882712.
PR 07-FEB-1994; 94US-00193627.
PR 08-NOV-1999; 99US-00436430.
PR 20-MAR-2000; 2000US-00531025.
PR 09-AUG-2000; 2000US-00636385.
PR 24-OCT-2000; 2000US-00696347.
PR 08-JUN-2001; 2001US-00877478.
PR 08-JUN-2001; 2001US-0296876P.
PR 24-OCT-2001; 2001US-0335059P.
PR 05-DEC-2001; 2001US-0337055P.
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
XX
PA (MORR/) MORRISSEY D.
PA (MCSW/) MCSWIGGEN J A.
PA (BEIG/) BEIGELMAN L.
XX
PI Morrissey D, Mcswiggen JA, Beigelman L;
XX
DR WPI; 2003-901032/82.
XX
PT New short interfering nucleic acid molecules which down-regulates
PT expression of a hepatitis B virus (HBV) or which inhibits HBV
PT replication, useful for treating human HBV infections or for
PT characterizing gene function.
XX
PS Claim 11; Page 41; 72pp; English.
XX
CC The invention relates to a short interfering nucleic acid (siNA) molecule
CC that down-regulates expression of a hepatitis B virus (HBV) gene by RNA
CC interference or that inhibits HBV replication. Also disclosed are the
CC following: (i) a method of modulating the expression of a HBV gene in a
CC tissue explant; (ii)) a method of generating a library of siNA constructs
CC having predetermined complexity; (iii) a cell containing one or more siNA
CC molecules; (iv)a kit containing a siNA molecule which can be used to
CC modulate the expression of a HBV target gene in a cell, tissue or
CC organism; and (v) a method for synthesising a siNA molecule. The siNA
CC molecule is adapted for use to treat HBV infection, and comprises a sense
CC and an antisense region, where the antisense region comprises sequence
CC complementary to an RNA sequence encoding HBV and the sense region
CC comprises sequence complementary to the antisense region. The siNA
CC molecule is assembled from 2 nucleic acid fragments, where one fragment
CC comprises the sense region and the second fragment comprises the
CC antisense region of the siNA molecule, where sense region and the
CC antisense region comprise separate oligonucleotides, and are covalently
CC connected via a linker molecule. The linker molecule is a polynucleotide
CC linker or a non-nucleotide linker. The sense region comprises a 3'-
CC terminal overhang and the antisense region comprises a 3'-terminal
CC overhang. The 3'-terminal overhangs each comprise about 2 nucleotides.
CC The antisense region 3'-terminal overhang is complementary to RNA
CC encoding HBV. The siNA is useful for treating human hepatitis B virus
CC infections, and for characterising pathways of gene function, e.g. to
CC inhibit activity of target genes in a pathway to determine the function
CC of uncharacterised genes in gene function analysis. The siNA molecules
CC may also be used in clinical, industrial, environmental, agricultural
CC and/or research settings. The present sequence represents 1 of 1504 HBV
CC siNA molecules of the invention.
XX
SQ Sequence 19 BP; 8 A; 7 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAAGGCA 16
||||||||||||||||
Db 1 AAAGCCACCCAAGGCA 16

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Job time : 279 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 29, 2005, 05:28:20 ; Search time 98 Seconds
(without alignments)
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Title: US-09-888-164-29
Perfect score: 16
Sequence: 1 aaagccacccaaggca 16

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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	16	100.0	16	1	US-08-281-106-48	Sequence 48, Appl
	2	16	100.0	16	4	US-09-199-269-48	Sequence 48, Appl
	3	16	100.0	16	4	US-09-155-885A-41	Sequence 41, Appl
	4	16	100.0	18	1	US-08-480-220A-22	Sequence 22, Appl
	5	16	100.0	18	2	US-08-864-404-22	Sequence 22, Appl
	6	16	100.0	18	4	US-09-155-885A-49	Sequence 49, Appl
c	7	16	100.0	19	1	US-08-480-220A-21	Sequence 21, Appl
c	8	16	100.0	19	1	US-08-480-220A-25	Sequence 25, Appl
c	9	16	100.0	19	2	US-08-864-404-21	Sequence 21, Appl
c	10	16	100.0	19	2	US-08-864-404-25	Sequence 25, Appl
	11	16	100.0	20	2	US-08-501-968-18	Sequence 18, Appl
	12	16	100.0	20	5	PCT-US96-10984-18	Sequence 18, Appl
	13	16	100.0	21	1	US-08-281-106-45	Sequence 45, Appl
	14	16	100.0	21	1	US-08-281-106-47	Sequence 47, Appl
	15	16	100.0	21	1	US-08-287-337A-5	Sequence 5, Appli
	16	16	100.0	21	2	US-08-501-968-7	Sequence 7, Appli
	17	16	100.0	21	4	US-09-199-269-45	Sequence 45, Appl
	18	16	100.0	21	4	US-09-199-269-47	Sequence 47, Appl
	19	16	100.0	21	5	PCT-US95-00508-5	Sequence 5, Appli
	20	16	100.0	21	5	PCT-US96-10984-7	Sequence 7, Appli
c	21	16	100.0	23	1	US-08-758-626-13	Sequence 13, Appl
c	22	16	100.0	23	5	PCT-US94-07684-13	Sequence 13, Appl
c	23	16	100.0	44	1	US-08-480-220A-19	Sequence 19, Appl
c	24	16	100.0	44	1	US-08-480-220A-20	Sequence 20, Appl
c	25	16	100.0	44	2	US-08-864-404-19	Sequence 19, Appl
c	26	16	100.0	44	2	US-08-864-404-20	Sequence 20, Appl
c	27	16	100.0	50	1	US-08-758-626-25	Sequence 25, Appl
c	28	16	100.0	50	5	PCT-US94-07684-25	Sequence 25, Appl
c	29	16	100.0	61	4	US-08-890-735C-3	Sequence 3, Appli
c	30	16	100.0	69	1	US-08-098-313-10	Sequence 10, Appl
c	31	16	100.0	69	5	PCT-US92-01188-10	Sequence 10, Appl
c	32	16	100.0	72	2	US-08-697-404-12	Sequence 12, Appl
c	33	16	100.0	81	1	US-08-287-337A-9	Sequence 9, Appli
c	34	16	100.0	114	3	US-08-075-520A-8	Sequence 8, Appli
c	35	16	100.0	291	3	US-08-075-520A-11	Sequence 11, Appl
c	36	16	100.0	390	3	US-08-075-520A-16	Sequence 16, Appl
c	37	16	100.0	477	3	US-08-445-585-2	Sequence 2, Appli
c	38	16	100.0	534	3	US-08-075-520A-4	Sequence 4, Appli
c	39	16	100.0	534	3	US-08-075-520A-5	Sequence 5, Appli
c	40	16	100.0	588	3	US-08-075-520A-35	Sequence 35, Appl
c	41	16	100.0	655	3	US-08-483-511-56	Sequence 56, Appl
c	42	16	100.0	655	5	PCT-US93-01009-56	Sequence 56, Appl
c	43	16	100.0	909	3	US-09-243-282-1	Sequence 1, Appli
c	44	16	100.0	2348	3	US-08-480-173A-42	Sequence 42, Appl
c	45	16	100.0	2348	3	US-08-484-408A-42	Sequence 42, Appl

ALIGNMENTS

```
RESULT 1
US-08-281-106-48
; Sequence 48, Application US/08281106
; Patent No. 5646262
;  GENERAL INFORMATION:
;    APPLICANT:  KORBA, Brent E.
;    APPLICANT:  GERIN, John L.
;    TITLE OF INVENTION:  Antisense Oligonucleotides Against
;    TITLE OF INVENTION:  Hepatitis B Viral Replication
;    NUMBER OF SEQUENCES:  56
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W.
;      CITY:  Washington, D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/281,106
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  66683/112/GEUN
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202 672 5300
;      TELEFAX:  202 672 5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  48:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    ANTI-SENSE:  YES
US-08-281-106-48

  Query Match           100.0%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity  100.0%;  Pred. No. 22;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16
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RESULT 2
US-09-199-269-48
; Sequence 48, Application US/09199269
; Patent No. 6503533
;   GENERAL INFORMATION:
;        APPLICANT: KORBA, Brent E.
;                   GERIN, John L.
;        TITLE OF INVENTION: Antisense Oligonucleotides Against
;                            Hepatitis B Viral Replication
;        NUMBER OF SEQUENCES: 56
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W.
;             CITY: Washington, D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/199,269
;             FILING DATE: 25-No. 6503533-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/281,106
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BENT, Stephen A.
;             REGISTRATION NUMBER: 29,768
;             REFERENCE/DOCKET NUMBER: 66683/112/GEUN
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202 672 5300
;             TELEFAX: 202 672 5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 48:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        ANTI-SENSE: YES
;        SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-09-199-269-48

  Query Match             100.0%;  Score 16;  DB 4;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 3
US-09-155-885A-41
; Sequence 41, Application US/09155885A
; Patent No. 6709812
;   GENERAL INFORMATION:
;        APPLICANT: STUYVER, LIEVEN
;                   ROSSAU, RUDI
;                   MAERTENS, GEERT
;        TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
;        NUMBER OF SEQUENCES: 313
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: NIXON & VANDERHYE P.C.
;             STREET: 1100 NORTH GLEBE ROAD
;             CITY: ARLINGTON
;             STATE: VIRGINIA
;             COUNTRY: U.S.A.
;             ZIP: 22201-4714
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/155,885A
;             FILING DATE: 08-Oct-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/EP97/02002
;             FILING DATE: 21-APR-1997
;             APPLICATION NUMBER: EP 96870053.4
;             FILING DATE: 19-APR-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SADOFF, B.J.
;             REGISTRATION NUMBER: 36,663
;             REFERENCE/DOCKET NUMBER: 2551-5
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (703) 816-4000
;             TELEFAX: (703) 816-4100
;   INFORMATION FOR SEQ ID NO: 41:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-09-155-885A-41

  Query Match             100.0%;  Score 16;  DB 4;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 4
US-08-480-220A-22
; Sequence 22, Application US/08480220A
; Patent No. 5667974
;  GENERAL INFORMATION:
;    APPLICANT:  Birkenmeyer, Larry
;    APPLICANT:  Mushahwar, Isa K.
;    TITLE OF INVENTION:  METHOD FOR DETECTING NUCLEIC ACID
;    TITLE OF INVENTION:  SEQUENCE USING COMPETITIVE AMPLIFICATION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories D377/AP6D
;      STREET:  100 Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC Compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,220A
;      FILING DATE:  07 JUN 1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Porembski, Priscilla E.
;      REGISTRATION NUMBER:  33,207
;      REFERENCE/DOCKET NUMBER:  5770.US.01
;    TELECOMMUNICATION INFORMATION:
```

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;      TELEPHONE:  708/937-6365
;      TELEFAX:  708/938-2623
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  synthetic DNA
;    FEATURE:
;      NAME/KEY:  5' phosphate
;      LOCATION:  1
;    FEATURE:
;      NAME/KEY:  3' fluorescein
;      LOCATION:  18
US-08-480-220A-22

  Query Match             100.0%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 5
US-08-864-404-22
; Sequence 22, Application US/08864404
; Patent No. 5955598
;  GENERAL INFORMATION:
;    APPLICANT:  Birkenmeyer, Larry
;    APPLICANT:  Mushahwar, Isa K.
;    TITLE OF INVENTION:  METHOD FOR DETECTING NUCLEIC ACID
;    TITLE OF INVENTION:  SEQUENCE USING COMPETITIVE AMPLIFICATION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories D377/AP6D
;      STREET:  100 Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60064-35008
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC Compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/864,404
;      FILING DATE:  28-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/480,220
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Porembski, Priscilla E.
;      REGISTRATION NUMBER:  33,207
;      REFERENCE/DOCKET NUMBER:  5770.US.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  708/937-6365
;      TELEFAX:  708/938-2623
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  synthetic DNA
;    FEATURE:
;      NAME/KEY:  5' phosphate
;      LOCATION:  1
;    FEATURE:
;      NAME/KEY:  3' fluorescein
;      LOCATION:  18
US-08-864-404-22

  Query Match             100.0%;  Score 16;  DB 2;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 6
US-09-155-885A-49
; Sequence 49, Application US/09155885A
; Patent No. 6709812
;  GENERAL INFORMATION:
;       APPLICANT: STUYVER, LIEVEN
;                  ROSSAU, RUDI
;                  MAERTENS, GEERT
;       TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
;       NUMBER OF SEQUENCES: 313
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: NIXON & VANDERHYE P.C.
;            STREET: 1100 NORTH GLEBE ROAD
;            CITY: ARLINGTON
;            STATE: VIRGINIA
;            COUNTRY: U.S.A.
;            ZIP: 22201-4714
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/155,885A
;            FILING DATE: 08-Oct-1998
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: PCT/EP97/02002
;            FILING DATE: 21-APR-1997
;            APPLICATION NUMBER: EP 96870053.4
;            FILING DATE: 19-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SADOFF, B.J.
;            REGISTRATION NUMBER: 36,663
;            REFERENCE/DOCKET NUMBER: 2551-5
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (703) 816-4000
;            TELEFAX: (703) 816-4100
;  INFORMATION FOR SEQ ID NO: 49:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 18 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
;       SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-09-155-885A-49

  Query Match             100.0%;  Score 16;  DB 4;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16
```

```
RESULT 7
US-08-480-220A-21/c
; Sequence 21, Application US/08480220A
; Patent No. 5667974
;  GENERAL INFORMATION:
;    APPLICANT:  Birkenmeyer, Larry
;    APPLICANT:  Mushahwar, Isa K.
;    TITLE OF INVENTION:  METHOD FOR DETECTING NUCLEIC ACID
;    TITLE OF INVENTION:  SEQUENCE USING COMPETITIVE AMPLIFICATION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories D377/AP6D
;      STREET:  100 Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC Compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,220A
;      FILING DATE:  07 JUN 1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Porembski, Priscilla E.
;      REGISTRATION NUMBER:  33,207
;      REFERENCE/DOCKET NUMBER:  5770.US.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  708/937-6365
;      TELEFAX:  708/938-2623
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  synthetic DNA
;    FEATURE:
;      NAME/KEY:  5' fluorescein
;      LOCATION:  1
US-08-480-220A-21

  Query Match             100.0%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         18 AAAGCCACCCAAGGCA 3


RESULT 8
US-08-480-220A-25/c
; Sequence 25, Application US/08480220A
; Patent No. 5667974
;  GENERAL INFORMATION:
;    APPLICANT:  Birkenmeyer, Larry
;    APPLICANT:  Mushahwar, Isa K.
;    TITLE OF INVENTION:  METHOD FOR DETECTING NUCLEIC ACID
;    TITLE OF INVENTION:  SEQUENCE USING COMPETITIVE AMPLIFICATION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories D377/AP6D
;      STREET:  100 Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC Compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,220A
;      FILING DATE:  07 JUN 1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Porembski, Priscilla E.
;      REGISTRATION NUMBER:  33,207
;      REFERENCE/DOCKET NUMBER:  5770.US.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  708/937-6365
;      TELEFAX:  708/938-2623
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  synthetic DNA
;    FEATURE:
;      NAME/KEY:  5' fluorescein
;      LOCATION:  1
US-08-480-220A-25

  Query Match             100.0%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         18 AAAGCCACCCAAGGCA 3


RESULT 9
US-08-864-404-21/c
; Sequence 21, Application US/08864404
; Patent No. 5955598
;  GENERAL INFORMATION:
;    APPLICANT:  Birkenmeyer, Larry
;    APPLICANT:  Mushahwar, Isa K.
;    TITLE OF INVENTION:  METHOD FOR DETECTING NUCLEIC ACID
;    TITLE OF INVENTION:  SEQUENCE USING COMPETITIVE AMPLIFICATION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories D377/AP6D
;      STREET:  100 Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60064-35008
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC Compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/864,404
;      FILING DATE:  28-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/480,220
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Porembski, Priscilla E.
;      REGISTRATION NUMBER:  33,207
;      REFERENCE/DOCKET NUMBER:  5770.US.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  708/937-6365
```

```
;       TELEFAX:  708/938-2623
;       TELEX:
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  19 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;    MOLECULE TYPE:  synthetic DNA
;    FEATURE:
;       NAME/KEY:  5' fluorescein
;       LOCATION:  1
US-08-864-404-21

  Query Match             100.0%;  Score 16;  DB 2;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         18 AAAGCCACCCAAGGCA 3


RESULT 10
US-08-864-404-25/c
; Sequence 25, Application US/08864404
; Patent No. 5955598
;  GENERAL INFORMATION:
;    APPLICANT:  Birkenmeyer, Larry
;    APPLICANT:  Mushahwar, Isa K.
;    TITLE OF INVENTION:  METHOD FOR DETECTING NUCLEIC ACID
;    TITLE OF INVENTION:  SEQUENCE USING COMPETITIVE AMPLIFICATION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Abbott Laboratories D377/AP6D
;       STREET:  100 Abbott Park Road
;       CITY:  Abbott Park
;       STATE:  Illinois
;       COUNTRY:  USA
;       ZIP:  60064-35008
;    COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC Compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/864,404
;       FILING DATE:  28-MAY-1997
;       CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/480,220
;       FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;       NAME:  Porembski, Priscilla E.
;       REGISTRATION NUMBER:  33,207
;       REFERENCE/DOCKET NUMBER:  5770.US.01
;    TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  708/937-6365
;       TELEFAX:  708/938-2623
;       TELEX:
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  19 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;    MOLECULE TYPE:  synthetic DNA
;    FEATURE:
;       NAME/KEY:  5' fluorescein
;       LOCATION:  1
US-08-864-404-25

  Query Match             100.0%;  Score 16;  DB 2;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         18 AAAGCCACCCAAGGCA 3


RESULT 11
US-08-501-968-18
; Sequence 18, Application US/08501968
; Patent No. 5985662
;  GENERAL INFORMATION:
;    APPLICANT:  Kevin Anderson and Lex Cowsert
;    TITLE OF INVENTION:  Antisense Inhibition of Hepatitis B
;    TITLE OF INVENTION:  Virus Replication
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Jane Massey Licata, Esq.
;       STREET:  210 Lake Drive East, Suite 201
;       CITY:  Cherry Hill
;       STATE:  NJ
;       COUNTRY:  USA
;       ZIP:  08002
;    COMPUTER READABLE FORM:
;       MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;       COMPUTER:  IBM 486
;       OPERATING SYSTEM:  WINDOWS FOR WORKGROUPS
;       SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/501,968
;       FILING DATE:  herewith
;       CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:  none
;    ATTORNEY/AGENT INFORMATION:
;       NAME:  Jane Massey Licata
;       REGISTRATION NUMBER:  32,257
;       REFERENCE/DOCKET NUMBER:  ISPH-0128
;    TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (609) 779-2400
;       TELEFAX:  (609) 779-8488
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  20 nucleotides
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  YES
US-08-501-968-18

  Query Match             100.0%;  Score 16;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 12
PCT-US96-10984-18
; Sequence 18, Application PC/TUS9610984
;  GENERAL INFORMATION:
;    APPLICANT:  Kevin Anderson and Lex Cowsert
;    TITLE OF INVENTION:  Antisense Inhibition of Hepatitis B
;    TITLE OF INVENTION:  Virus Replication
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Jane Massey Licata, Esq.
;       STREET:  210 Lake Drive East, Suite 201
;       CITY:  Cherry Hill
;       STATE:  NJ
```

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;       COUNTRY:  USA
;       ZIP:  08002
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 Mb
;       MEDIUM TYPE:  STORAGE
;       COMPUTER:  IBM 486
;       OPERATING SYSTEM:  WINDOWS FOR WORKGROUPS
;       SOFTWARE:  WORDPERFECT 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US96/10984
;       FILING DATE:  herewith
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:  none
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Jane Massey Licata
;       REGISTRATION NUMBER:  32,257
;       REFERENCE/DOCKET NUMBER:  ISPH-0128
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (609) 779-2400
;       TELEFAX:  (609) 779-8488
;   INFORMATION FOR SEQ ID NO:  18:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  20 nucleotides
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  YES
PCT-US96-10984-18

  Query Match             100.0%;  Score 16;  DB 5;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 13
US-08-281-106-45
; Sequence 45, Application US/08281106
; Patent No. 5646262
;  GENERAL INFORMATION:
;    APPLICANT:  KORBA, Brent E.
;    APPLICANT:  GERIN, John L.
;    TITLE OF INVENTION:  Antisense Oligonucleotides Against
;    TITLE OF INVENTION:  Hepatitis B Viral Replication
;    NUMBER OF SEQUENCES:  56
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W.
;      CITY:  Washington, D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/281,106
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  66683/112/GEUN
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202 672 5300
;      TELEFAX:  202 672 5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  45:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    ANTI-SENSE:  YES
US-08-281-106-45

  Query Match             100.0%;  Score 16;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 14
US-08-281-106-47
; Sequence 47, Application US/08281106
; Patent No. 5646262
;  GENERAL INFORMATION:
;    APPLICANT:  KORBA, Brent E.
;    APPLICANT:  GERIN, John L.
;    TITLE OF INVENTION:  Antisense Oligonucleotides Against
;    TITLE OF INVENTION:  Hepatitis B Viral Replication
;    NUMBER OF SEQUENCES:  56
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W.
;      CITY:  Washington, D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/281,106
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  66683/112/GEUN
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202 672 5300
;      TELEFAX:  202 672 5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  47:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    ANTI-SENSE:  YES
US-08-281-106-47

  Query Match             100.0%;  Score 16;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          6 AAAGCCACCCAAGGCA 21


RESULT 15
US-08-287-337A-5
; Sequence 5, Application US/08287337A
; Patent No. 5728518
;  GENERAL INFORMATION:
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;    APPLICANT:  Ellen Carmichael
;    TITLE OF INVENTION:  ANTIVIRAL OLIGONUCLOETIDE
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street, Suite 510
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/287,337A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Giulio A. DeConti, Jr.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  TTI-109
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-287-337A-5

  Query Match           100.0%;  Score 16;  DB 1;  Length 21;
  Best Local Similarity  100.0%;  Pred. No. 23;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          6 AAAGCCACCCAAGGCA 21


Search completed: March 29, 2005, 07:38:03
Job time : 103 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 29, 2005, 07:36:34 ; Search time 322 Seconds
(without alignments)
296.116 Million cell updates/sec

Title: US-09-888-164-29
Perfect score: 16
Sequence: 1 aaagccacccaaggca 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5552208 seqs, 2979665951 residues

Total number of hits satisfying chosen parameters: 11104416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
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21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	16	100.0	16	10	US-09-888-164-29	Sequence 29, Appl
2	16	100.0	16	17	US-10-453-792-41	Sequence 41, Appl
c 3	16	100.0	17	10	US-09-877-478-1755	Sequence 1755, Ap
c 4	16	100.0	17	10	US-09-877-478-2378	Sequence 2378, Ap
c 5	16	100.0	17	17	US-10-342-902-1755	Sequence 1755, Ap
c 6	16	100.0	17	17	US-10-342-902-2378	Sequence 2378, Ap
c 7	16	100.0	17	18	US-10-669-841-1755	Sequence 1755, Ap
c 8	16	100.0	17	18	US-10-669-841-2181	Sequence 2181, Ap
9	16	100.0	18	17	US-10-453-792-49	Sequence 49, Appl
c 10	16	100.0	19	17	US-10-244-647-54	Sequence 54, Appl
c 11	16	100.0	19	17	US-10-244-647-574	Sequence 574, App
c 12	16	100.0	19	17	US-10-244-647-576	Sequence 576, App
c 13	16	100.0	19	17	US-10-244-647-577	Sequence 577, App
14	16	100.0	19	17	US-10-244-647-700	Sequence 700, App
15	16	100.0	19	17	US-10-244-647-1220	Sequence 1220, Ap
16	16	100.0	19	17	US-10-244-647-1222	Sequence 1222, Ap
17	16	100.0	19	17	US-10-244-647-1223	Sequence 1223, Ap
c 18	16	100.0	23	17	US-10-244-647-1296	Sequence 1296, Ap
c 19	16	100.0	54	9	US-09-756-500-4	Sequence 4, Appli
c 20	16	100.0	114	17	US-10-394-896-8	Sequence 8, Appli
c 21	16	100.0	291	17	US-10-394-896-11	Sequence 11, Appl
c 22	16	100.0	390	17	US-10-394-896-16	Sequence 16, Appl
c 23	16	100.0	534	17	US-10-394-896-4	Sequence 4, Appli
c 24	16	100.0	534	17	US-10-394-896-5	Sequence 5, Appli
c 25	16	100.0	560	19	US-10-478-633A-69	Sequence 69, Appl
c 26	16	100.0	560	19	US-10-478-633A-70	Sequence 70, Appl
c 27	16	100.0	588	17	US-10-394-896-35	Sequence 35, Appl
c 28	16	100.0	639	17	US-10-312-045-1	Sequence 1, Appli
c 29	16	100.0	639	18	US-10-240-917-1	Sequence 1, Appli
c 30	16	100.0	655	9	US-09-912-679-56	Sequence 56, Appl
c 31	16	100.0	655	9	US-09-466-035-56	Sequence 56, Appl
c 32	16	100.0	655	11	US-09-821-662-23	Sequence 23, Appl
33	16	100.0	1841	17	US-10-398-221-3305	Sequence 3305, Ap
c 34	16	100.0	1977	17	US-10-461-790-97	Sequence 97, Appl
c 35	16	100.0	3161	17	US-10-453-792-301	Sequence 301, App
c 36	16	100.0	3182	9	US-09-929-955-14	Sequence 14, Appl
c 37	16	100.0	3182	13	US-10-104-966-14	Sequence 14, Appl
c 38	16	100.0	3182	17	US-10-453-792-302	Sequence 302, App
c 39	16	100.0	3182	17	US-10-453-792-303	Sequence 303, App
c 40	16	100.0	3182	17	US-10-453-792-304	Sequence 304, App
c 41	16	100.0	3182	17	US-10-453-792-305	Sequence 305, App
c 42	16	100.0	3182	17	US-10-453-792-306	Sequence 306, App
c 43	16	100.0	3182	17	US-10-453-792-307	Sequence 307, App
c 44	16	100.0	3182	17	US-10-453-792-308	Sequence 308, App
c 45	16	100.0	3182	17	US-10-719-619-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-888-164-29
; Sequence 29, Application US/09888164
; Publication No. US20030119724A1
; GENERAL INFORMATION:
; APPLICANT: Ts'o, Paul O.P.
; APPLICANT: Hangeland, Jon
; APPLICANT: Deamond, Scott
; APPLICANT: Roby, Clinton
; TITLE OF INVENTION: LIGANDS TO ENHANCE CELLULAR UPTAKE OF BIOMOLECULES
; FILE REFERENCE: 212241
; CURRENT APPLICATION NUMBER: US/09/888,164
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 09/282,455
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 08/755,062
; PRIOR FILING DATE: 1996-11-22
; PRIOR APPLICATION NUMBER: 60/007,480
; PRIOR FILING DATE: 1995-11-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Control oligomer
US-09-888-164-29

Query Match 100.0%; Score 16; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAAGGCA 16

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              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 2
US-10-453-792-41
; Sequence 41, Application US/10453792
; Publication No. US20040029110A1
;  GENERAL INFORMATION:
;       APPLICANT: STUYVER, LIEVEN
;                  ROSSAU, RUDI
;                  MAERTENS, GEERT
;       TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
;       NUMBER OF SEQUENCES: 313
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: NIXON & VANDERHYE P.C.
;            STREET: 1100 NORTH GLEBE ROAD
;            CITY: ARLINGTON
;            STATE: VIRGINIA
;            COUNTRY: U.S.A.
;            ZIP: 22201-4714
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/453,792
;            FILING DATE: 04-Jun-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/155,885A
;            FILING DATE: 08-Oct-1998
;            APPLICATION NUMBER: PCT/EP97/02002
;            FILING DATE: 21-APR-1997
;            APPLICATION NUMBER: EP 96870053.4
;            FILING DATE: 19-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SADOFF, B.J.
;            REGISTRATION NUMBER: 36,663
;            REFERENCE/DOCKET NUMBER: 2551-5
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (703) 816-4000
;            TELEFAX: (703) 816-4100
;   INFORMATION FOR SEQ ID NO: 41:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 16 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
;       SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-453-792-41

  Query Match             100.0%;  Score 16;  DB 17;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 3
US-09-877-478-1755/c
; Sequence 1755, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Draper, Kenneth
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Morrissey, Dave
;  TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
;  FILE REFERENCE: MBHB00-845-H (400/029)
;  CURRENT APPLICATION NUMBER: US/09/877,478
;  CURRENT FILING DATE:  2001-12-31
;  PRIOR APPLICATION NUMBER: US 07/882,712
;  PRIOR FILING DATE: 1992-05-14
;  PRIOR APPLICATION NUMBER: US 09/531,025
;  PRIOR FILING DATE: 2000-03-20
;  PRIOR APPLICATION NUMBER: US 09/636,385
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: US 09/696,347
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 08/193,627
;  PRIOR FILING DATE: 1994-02-07
;  PRIOR APPLICATION NUMBER: US 08/433,993
;  PRIOR FILING DATE: 1995-05-04
;  PRIOR APPLICATION NUMBER: US 08/434,504
;  PRIOR FILING DATE: 1995-05-04
;  PRIOR APPLICATION NUMBER: US 09/436,430
;  PRIOR FILING DATE: 1999-11-08
;  NUMBER OF SEQ ID NOS: 6586
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1755
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Hepatitis B virus
US-09-877-478-1755

  Query Match             100.0%;  Score 16;  DB 10;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         16 AAAGCCACCCAAGGCA 1


RESULT 4
US-09-877-478-2378/c
; Sequence 2378, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Draper, Kenneth
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Morrissey, Dave
;  TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
;  FILE REFERENCE: MBHB00-845-H (400/029)
;  CURRENT APPLICATION NUMBER: US/09/877,478
;  CURRENT FILING DATE:  2001-12-31
;  PRIOR APPLICATION NUMBER: US 07/882,712
;  PRIOR FILING DATE: 1992-05-14
;  PRIOR APPLICATION NUMBER: US 09/531,025
;  PRIOR FILING DATE: 2000-03-20
;  PRIOR APPLICATION NUMBER: US 09/636,385
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: US 09/696,347
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 08/193,627
;  PRIOR FILING DATE: 1994-02-07
;  PRIOR APPLICATION NUMBER: US 08/433,993
;  PRIOR FILING DATE: 1995-05-04
;  PRIOR APPLICATION NUMBER: US 08/434,504
;  PRIOR FILING DATE: 1995-05-04
;  PRIOR APPLICATION NUMBER: US 09/436,430
;  PRIOR FILING DATE: 1999-11-08
;  NUMBER OF SEQ ID NOS: 6586
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2378
;   LENGTH: 17
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;   TYPE: RNA
;   ORGANISM: Hepatitis B virus
US-09-877-478-2378

  Query Match             100.0%;  Score 16;  DB 10;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         17 AAAGCCACCCAAGGCA 2


RESULT 5
US-10-342-902-1755/c
; Sequence 1755, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  Draper, Kenneth
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Morrissey, Dave
;  TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
;  FILE REFERENCE: 400/075 (MBHB00-845-I)
;  CURRENT APPLICATION NUMBER: US/10/342,902
;  CURRENT FILING DATE:  2003-01-15
;  PRIOR APPLICATION NUMBER: US 09/877,478
;  PRIOR FILING DATE: 2001-06-08
;  PRIOR APPLICATION NUMBER: US 09/531,025
;  PRIOR FILING DATE: 2000-03-20
;  PRIOR APPLICATION NUMBER: US 09/636,385
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: US 09/696,347
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 08/193,627
;  PRIOR FILING DATE: 1994-02-07
;  PRIOR APPLICATION NUMBER: US 07/882,712
;  PRIOR FILING DATE: 1992-05-14
;  PRIOR APPLICATION NUMBER: US 09/436,430
;  PRIOR FILING DATE: 1999-11-08
;  NUMBER OF SEQ ID NOS: 6592
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1755
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Hepatitis B virus
US-10-342-902-1755

  Query Match             100.0%;  Score 16;  DB 17;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         16 AAAGCCACCCAAGGCA 1


RESULT 6
US-10-342-902-2378/c
; Sequence 2378, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  Draper, Kenneth
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Morrissey, Dave
;  TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
;  FILE REFERENCE: 400/075 (MBHB00-845-I)
;  CURRENT APPLICATION NUMBER: US/10/342,902
;  CURRENT FILING DATE:  2003-01-15
;  PRIOR APPLICATION NUMBER: US 09/877,478
;  PRIOR FILING DATE: 2001-06-08
;  PRIOR APPLICATION NUMBER: US 09/531,025
;  PRIOR FILING DATE: 2000-03-20
;  PRIOR APPLICATION NUMBER: US 09/636,385
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: US 09/696,347
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 08/193,627
;  PRIOR FILING DATE: 1994-02-07
;  PRIOR APPLICATION NUMBER: US 07/882,712
;  PRIOR FILING DATE: 1992-05-14
;  PRIOR APPLICATION NUMBER: US 09/436,430
;  PRIOR FILING DATE: 1999-11-08
;  NUMBER OF SEQ ID NOS: 6592
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2378
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Hepatitis B virus
US-10-342-902-2378

  Query Match             100.0%;  Score 16;  DB 17;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         17 AAAGCCACCCAAGGCA 2


RESULT 7
US-10-669-841-1755/c
; Sequence 1755, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  Lawrence, Blatt
;  APPLICANT:  Dennis, Macejak
;  APPLICANT:  James, McSwiggen
;  APPLICANT:  David, Morrissey
;  APPLICANT:  Pamela, Pavco
;  APPLICANT:  Patrice, Lee
;  APPLICANT:  Kenneth, Draper
;  APPLICANT:  Elisabeth, Roberts
;  TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA
;  TITLE OF INVENTION:  VIRUS REPLICATION
;  FILE REFERENCE: 400/042US  (MBHB02-249-E)
;  CURRENT APPLICATION NUMBER: US/10/669,841
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: PCT/US02/09187
;  PRIOR FILING DATE: 2002-03-26
;  PRIOR APPLICATION NUMBER: US 60/296,876
;  PRIOR FILING DATE: 2001-06-08
;  PRIOR APPLICATION NUMBER: US 60/335,059
;  PRIOR FILING DATE: 2001-10-24
;  PRIOR APPLICATION NUMBER: US 60/337,055
;  PRIOR FILING DATE: 2001-12-05
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/363,124
;  PRIOR FILING DATE: 2002-03-11
;  PRIOR APPLICATION NUMBER: US 09/817,879
;  PRIOR FILING DATE: 2001-03-26
;  PRIOR APPLICATION NUMBER: US 09/740,332
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: US 09/611,931
;  PRIOR FILING DATE: 2000-07-07
;  PRIOR APPLICATION NUMBER: US 09/504,321
;  PRIOR FILING DATE: 2000-02-15
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 16207
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1755
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;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Hepatitis B Virus
US-10-669-841-1755

  Query Match             100.0%;  Score 16;  DB 18;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         16 AAAGCCACCCAAGGCA 1


RESULT 8
US-10-669-841-2181/c
; Sequence 2181, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  Lawrence, Blatt
;  APPLICANT:  Dennis, Macejak
;  APPLICANT:  James, McSwiggen
;  APPLICANT:  David, Morrissey
;  APPLICANT:  Pamela, Pavco
;  APPLICANT:  Patrice, Lee
;  APPLICANT:  Kenneth, Draper
;  APPLICANT:  Elisabeth, Roberts
;  TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA
;  TITLE OF INVENTION:  VIRUS REPLICATION
;  FILE REFERENCE: 400/042US  (MBHB02-249-E)
;  CURRENT APPLICATION NUMBER: US/10/669,841
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: PCT/US02/09187
;  PRIOR FILING DATE: 2002-03-26
;  PRIOR APPLICATION NUMBER: US 60/296,876
;  PRIOR FILING DATE: 2001-06-08
;  PRIOR APPLICATION NUMBER: US 60/335,059
;  PRIOR FILING DATE: 2001-10-24
;  PRIOR APPLICATION NUMBER: US 60/337,055
;  PRIOR FILING DATE: 2001-12-05
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/363,124
;  PRIOR FILING DATE: 2002-03-11
;  PRIOR APPLICATION NUMBER: US 09/817,879
;  PRIOR FILING DATE: 2001-03-26
;  PRIOR APPLICATION NUMBER: US 09/740,332
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: US 09/611,931
;  PRIOR FILING DATE: 2000-07-07
;  PRIOR APPLICATION NUMBER: US 09/504,321
;  PRIOR FILING DATE: 2000-02-15
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 16207
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2181
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Hepatitis B Virus
US-10-669-841-2181

  Query Match             100.0%;  Score 16;  DB 18;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         17 AAAGCCACCCAAGGCA 2


RESULT 9
US-10-453-792-49
; Sequence 49, Application US/10453792
; Publication No. US20040029110A1
;  GENERAL INFORMATION:
;       APPLICANT: STUYVER, LIEVEN
;                  ROSSAU, RUDI
;                  MAERTENS, GEERT
;       TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
;       NUMBER OF SEQUENCES: 313
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: NIXON & VANDERHYE P.C.
;            STREET: 1100 NORTH GLEBE ROAD
;            CITY: ARLINGTON
;            STATE: VIRGINIA
;            COUNTRY: U.S.A.
;            ZIP: 22201-4714
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/453,792
;            FILING DATE: 04-Jun-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/155,885A
;            FILING DATE: 08-Oct-1998
;            APPLICATION NUMBER: PCT/EP97/02002
;            FILING DATE: 21-APR-1997
;            APPLICATION NUMBER: EP 96870053.4
;            FILING DATE: 19-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SADOFF, B.J.
;            REGISTRATION NUMBER: 36,663
;            REFERENCE/DOCKET NUMBER: 2551-5
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (703) 816-4000
;            TELEFAX: (703) 816-4100
;   INFORMATION FOR SEQ ID NO: 49:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 18 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
;       SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-453-792-49

  Query Match             100.0%;  Score 16;  DB 17;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 10
US-10-244-647-54/c
; Sequence 54, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceutical, Inc.
;  APPLICANT:  Morrissey, David
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV) U
;  TITLE OF INVENTION:  Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/060 (MBHB02-1000)
;  CURRENT APPLICATION NUMBER: US/10/244,647
;  CURRENT FILING DATE:  2003-04-14
```

```
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/393,924
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: PCT US02/09187
;  PRIOR FILING DATE: 2002-03-26
;  PRIOR APPLICATION NUMBER: US 60/296,876
;  PRIOR FILING DATE: 2001-06-08
;  NUMBER OF SEQ ID NOS: 1524
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 54
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target sequence/siNA sense r
US-10-244-647-54

  Query Match           100.0%;  Score 16;  DB 17;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         19 AAAGCCACCCAAGGCA 4


RESULT 11
US-10-244-647-574/c
; Sequence 574, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceutical, Inc.
;  APPLICANT:  Morrissey, David
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV) U
;  TITLE OF INVENTION:  Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/060 (MBHB02-1000)
;  CURRENT APPLICATION NUMBER: US/10/244,647
;  CURRENT FILING DATE:  2003-04-14
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/393,924
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: PCT US02/09187
;  PRIOR FILING DATE: 2002-03-26
;  PRIOR APPLICATION NUMBER: US 60/296,876
;  PRIOR FILING DATE: 2001-06-08
;  NUMBER OF SEQ ID NOS: 1524
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 574
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target sequence/siNA sense r
US-10-244-647-574

  Query Match           100.0%;  Score 16;  DB 17;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         17 AAAGCCACCCAAGGCA 2


RESULT 12
US-10-244-647-576/c
; Sequence 576, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceutical, Inc.
;  APPLICANT:  Morrissey, David
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV) U
;  TITLE OF INVENTION:  Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/060 (MBHB02-1000)
;  CURRENT APPLICATION NUMBER: US/10/244,647
;  CURRENT FILING DATE:  2003-04-14
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/393,924
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: PCT US02/09187
;  PRIOR FILING DATE: 2002-03-26
;  PRIOR APPLICATION NUMBER: US 60/296,876
;  PRIOR FILING DATE: 2001-06-08
;  NUMBER OF SEQ ID NOS: 1524
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 576
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target sequence/siNA sense r
US-10-244-647-576

  Query Match           100.0%;  Score 16;  DB 17;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         16 AAAGCCACCCAAGGCA 1


RESULT 13
US-10-244-647-577/c
; Sequence 577, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceutical, Inc.
;  APPLICANT:  Morrissey, David
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV) U
;  TITLE OF INVENTION:  Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/060 (MBHB02-1000)
;  CURRENT APPLICATION NUMBER: US/10/244,647
;  CURRENT FILING DATE:  2003-04-14
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/393,924
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: PCT US02/09187
;  PRIOR FILING DATE: 2002-03-26
;  PRIOR APPLICATION NUMBER: US 60/296,876
;  PRIOR FILING DATE: 2001-06-08
;  NUMBER OF SEQ ID NOS: 1524
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 577
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target sequence/siNA sense r
US-10-244-647-577

  Query Match           100.0%;  Score 16;  DB 17;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
```

```
                  ||||||||||||||||
Db          18 AAAGCCACCCAAGGCA 3


RESULT 14
US-10-244-647-700
; Sequence 700, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceutical, Inc.
;  APPLICANT:  Morrissey, David
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV) U
;  TITLE OF INVENTION:  Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/060 (MBHB02-1000)
;  CURRENT APPLICATION NUMBER: US/10/244,647
;  CURRENT FILING DATE:  2003-04-14
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/393,924
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: PCT US02/09187
;  PRIOR FILING DATE: 2002-03-26
;  PRIOR APPLICATION NUMBER: US 60/296,876
;  PRIOR FILING DATE: 2001-06-08
;  NUMBER OF SEQ ID NOS: 1524
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 700
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-244-647-700

  Query Match             100.0%;  Score 16;  DB 17;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
                ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 15
US-10-244-647-1220
; Sequence 1220, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceutical, Inc.
;  APPLICANT:  Morrissey, David
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV) U
;  TITLE OF INVENTION:  Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/060 (MBHB02-1000)
;  CURRENT APPLICATION NUMBER: US/10/244,647
;  CURRENT FILING DATE:  2003-04-14
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/393,924
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: PCT US02/09187
;  PRIOR FILING DATE: 2002-03-26
;  PRIOR APPLICATION NUMBER: US 60/296,876
;  PRIOR FILING DATE: 2001-06-08
;  NUMBER OF SEQ ID NOS: 1524
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1220
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-244-647-1220

  Query Match             100.0%;  Score 16;  DB 17;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
                ||||||||||||||||
Db          3 AAAGCCACCCAAGGCA 18


Search completed: March 29, 2005, 08:34:46
Job time : 325 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 29, 2005, 05:05:15 ; Search time 2023 Seconds
(without alignments)
301.052 Million cell updates/sec

Title: US-09-888-164-29
Perfect score: 16
Sequence: 1 aaagccacccaaggca 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	16	100.0	384	2	BF327943	QV0-BN014
2	16	100.0	396	4	BI049449	CM2-GN029
3	16	100.0	441	9	CE327035	tigr-gss-
c 4	16	100.0	464	1	AA103554	mo24h10.r
5	16	100.0	496	2	BE144757	CM0-HT018
6	16	100.0	587	7	CF755881	DSAF1_2_A
c 7	16	100.0	623	5	BQ385327	NISC_mn11
8	16	100.0	646	6	CA192813	SCRLSB104
c 9	16	100.0	659	2	BB545848	BB545848
10	16	100.0	666	6	CA083440	SCEPAM201
c 11	16	100.0	700	1	AV359761	AV359761
c 12	16	100.0	770	6	CD778583	EST649944
13	16	100.0	895	4	BI250824	602993448
c 14	16	100.0	975	6	CA474404	AGENCOURT
c 15	16	100.0	987	7	W34362	W34362 ma99b12.r1
c 16	16	100.0	1684	9	CG754259	P049-3-E1
c 17	16	100.0	2005	3	AK009491	Mus muscu
c 18	16	100.0	2368	3	AK078669	AK078669 Mus muscu
19	15	93.8	231	2	BB198017	BB198017
20	15	93.8	268	2	BF924007	CM2-NT017
21	15	93.8	285	2	BB090939	BB090939
c 22	15	93.8	287	2	BB309456	BB309456
23	15	93.8	294	7	W40391	W40391 zc80e10.r1
24	15	93.8	306	4	BI036238	BI036238 CM3-NT024
25	15	93.8	310	2	BB251202	BB251202 BB251202
c 26	15	93.8	323	1	AI812549	AI812549 12G1 Pine
27	15	93.8	328	2	AW921312	AW921312 EST352616
28	15	93.8	362	2	BF935524	BF935524 IL2-NT020
29	15	93.8	365	7	CV001930	CV001930 csa02-2ms
30	15	93.8	375	6	CB691996	CB691996 AMGNNUC:S
c 31	15	93.8	394	9	CE698527	CE698527 tigr-gss-
c 32	15	93.8	401	9	CE047936	CE047936 tigr-gss-
33	15	93.8	408	4	BI536031	BI536031 390188 MA
34	15	93.8	417	1	AA053186	AA053186 zl72a04.r
c 35	15	93.8	419	5	BQ198462	BQ198462 NXLV131_E
36	15	93.8	423	1	AA147417	AA147417 zo39e07.r
37	15	93.8	448	7	CN125873	CN125873 RHOH1_13_
38	15	93.8	455	6	CA902085	CA902085 PCS04956
39	15	93.8	459	1	AA205003	AA205003 zq72e12.r
c 40	15	93.8	495	8	BZ180217	BZ180217 CH230-485
c 41	15	93.8	499	7	CF477353	CF477353 RTWW3_7_B
c 42	15	93.8	502	9	CE812092	CE812092 tigr-gss-
43	15	93.8	509	6	CA902086	CA902086 PCSC10343
c 44	15	93.8	511	4	BG982671	BG982671 IL5-CN006
c 45	15	93.8	513	9	CE514588	CE514588 tigr-gss-

ALIGNMENTS

RESULT 1
BF327943
LOCUS BF327943 384 bp mRNA linear EST 22-NOV-2000
DEFINITION QV0-BN0148-070700-293-a12 BN0148 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF327943
VERSION BF327943.1 GI:11298691
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 384)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV0&t2=QV0-BN0148-070700-293-a12&t3=2000-07-07&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 41
High quality sequence stop: 382.
FEATURES Location/Qualifiers
source 1. .384
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BN0148"
/note="Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 16; DB 2; Length 384;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         16 AAAGCCACCCAAGGCA 31
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RESULT 2
BI049449
LOCUS BI049449 396 bp mRNA linear EST 15-JUN-2001
DEFINITION CM2-GN0295-020101-655-a07 GN0295 Homo sapiens cDNA, mRNA sequence.
ACCESSION BI049449
VERSION BI049449.1 GI:14456979
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 396)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM2&t2=CM2-GN0295-020101-655-a07&t3=2001-01-02&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 396.
FEATURES Location/Qualifiers
source 1. .396
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="GN0295"
/note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 16; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db        148 AAAGCCACCCAAGGCA 163
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RESULT 3
CE327035
LOCUS CE327035 441 bp DNA linear GSS 26-SEP-2003
DEFINITION tigr-gss-dog-17000333941473 Dog Library Canis familiaris genomic, genomic survey sequence.
ACCESSION CE327035
VERSION CE327035.1 GI:36139166
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 441)
AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K., Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
FEATURES Location/Qualifiers
source 1. .441
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site_1: BstXI; Libraries were prepared from peripheral blood"

ORIGIN

Query Match 100.0%; Score 16; DB 9; Length 441;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         73 AAAGCCACCCAAGGCA 88
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RESULT 4
AA103554/c
LOCUS AA103554 464 bp mRNA linear EST 29-OCT-1996
DEFINITION mo24h10.r1 Life Tech mouse embryo 13 5dpc 10666014 Mus musculus cDNA clone IMAGE:554563 5', mRNA sequence.
ACCESSION AA103554
VERSION AA103554.1 GI:1649714
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 464)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project

```
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:335355
            Putative full length read
            vector to vector length is 510
            Seq primer: -28M13 rev1 from Amersham.
FEATURES             Location/Qualifiers
     source          1. .464
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:554563"
                     /tissue_type="embryo"
                     /dev_stage="13.5dpc embryos"
                     /lab_host="DH10B"
                     /clone_lib="Life Tech mouse embryo 13 5dpc 10666014"
                     /note="Organ: whole embryo; Vector: pCMV-SPORT2; Site_1:
                     SalI; Site_2: NotI; Cloned unidirectionally.  Primer:
                     Oligo dT.  13.5dpc embryos. pCMV-SPORT2 vector."
ORIGIN

  Query Match             100.0%;  Score 16;  DB 1;  Length 464;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db        275 AAAGCCACCCAAGGCA 260


RESULT 5
BE144757
LOCUS       BE144757                 496 bp    mRNA    linear   EST 21-JUN-2000
DEFINITION  CM0-HT0180-041099-065-c06 HT0180 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE144757
VERSION     BE144757.1  GI:8607481
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 496)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=CM0-HT0180-041
            099-065-c06&t3=1999-10-04&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 496.
FEATURES             Location/Qualifiers
     source          1. .496
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="HT0180"
                     /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

  Query Match             100.0%;  Score 16;  DB 2;  Length 496;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db        229 AAAGCCACCCAAGGCA 244


RESULT 6
CF755881
LOCUS       CF755881                 587 bp    mRNA    linear   EST 17-OCT-2003
DEFINITION  DSAF1_2_A12.b1_A011 Drought-stressed after flowering Sorghum
            bicolor cDNA clone DSAF1_2_A12_A011 5', mRNA sequence.
ACCESSION   CF755881
VERSION     CF755881.1  GI:37704961
KEYWORDS    EST.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 587)
  AUTHORS   Cordonnier-Pratt,M.-M., Zhang,D., McCartor,K., Nguyen,H.T. and
            Pratt,L.H.
  TITLE     An EST Database from Sorghum: Subtracted post-flowering drought
            stressed leaf tissues
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Cordonnier-Pratt MM
            Laboratory for Genomics and Bioinformatics
            The University of Georgia, Department of Plant Biology
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 583 0210
            Email: mmpratt@uga.edu
            Library constructed at Texas Tech University by Deshui Zhang and
            Jianhang Jia in the laboratory of Dr. Henry Nguyen. Sequencing was
            done in the Laboratory for Genomics and Bioinformatics, University
            of Georgia. Sequence ends have been trimmed to exclude vector and
            regions below Phred quality 16. Three-prime sequences are presented
            as their reverse complement and have been trimmed to exclude polyA.
            Seq primer: JENREV (CAGGAAACAGCTATGACC).
FEATURES             Location/Qualifiers
     source          1. .587
                     /organism="Sorghum bicolor"
                     /mol_type="mRNA"
                     /cultivar="B35"
                     /db_xref="taxon:4558"
                     /clone="DSAF1_2_A12_A011"
                     /dev_stage="Post-flowering"
                     /lab_host="ElectroMax DH10B (BRL)"
                     /clone_lib="Drought-stressed after flowering"
                     /note="Organ: Leaf; Vector: pBlueScriptSK-; Site_1: XhoI;
                     Site_2: EcoRI; The library was prepared from polyA+ RNA
```

from leaves harvested from post-flowering, drought-stressed Sorghum bicolor, cv. B35. Double-stranded cDNA was cloned unidirectionally using the UniZap system from Stratagene. After amplification, the library was subtracted by re-association hybridization. Inserts can be excised with XhoI and EcoRI."

ORIGIN

Query Match 100.0%; Score 16; DB 7; Length 587;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAAGGCA 16
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Db 225 AAAGCCACCCAAGGCA 240

RESULT 7
BQ385327/c
LOCUS BQ385327 623 bp mRNA linear EST 22-MAY-2002
DEFINITION NISC_mn11f10.y1 NICHD_XGC_Ov1 Xenopus laevis cDNA clone IMAGE:5073186 5', mRNA sequence.
ACCESSION BQ385327
VERSION BQ385327.1 GI:21073014
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.
REFERENCE 1 (bases 1 to 623)
AUTHORS NIH-XCG http://image.llnl.gov/image/html/xenopuslib_info.shtml.
TITLE National Institute of Child Health and Human Development, National Cancer Insitute, Xenopus Gene Collection
JOURNAL Unpublished (2002)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation:
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Plate: LLAM11196 row: L column: 19
Seq primer: M13RP1 reverse primer (ABI).
FEATURES Location/Qualifiers
source 1. .623
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:5073186"
/sex="female"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD_XGC_Ov1"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.0 kb. Constructed by Life Technologies."
ORIGIN

Query Match 100.0%; Score 16; DB 5; Length 623;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAAGGCA 16
||||||||||||||||
Db 519 AAAGCCACCCAAGGCA 504

RESULT 8
CA192813
LOCUS CA192813 646 bp mRNA linear EST 24-SEP-2003
DEFINITION SCRLSB1042G03.g SB1 Saccharum officinarum cDNA clone SCRLSB1042G03 5', mRNA sequence.
ACCESSION CA192813
VERSION CA192813.1 GI:35139355
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.
REFERENCE 1 (bases 1 to 646)
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
Plate: 042 row: G column: 03
Seq primer: T7 Promoter Primer.
FEATURES Location/Qualifiers
source 1. .646
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCRLSB1042G03"
/lab_host="DH10B"
/clone_lib="SB1"
/note="Organ: Stalk Bark from adult plants; Vector: pSport1; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from [Stalk Bark from adult plants]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
ORIGIN

Query Match 100.0%; Score 16; DB 6; Length 646;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAAGGCA 16
||||||||||||||||
Db 63 AAAGCCACCCAAGGCA 78

RESULT 9
BB545848/c
LOCUS BB545848 659 bp mRNA linear EST 26-OCT-2001
DEFINITION BB545848 RIKEN full-length enriched, 0 day neonate eyeball Mus musculus cDNA clone E130306O04 3', mRNA sequence.
ACCESSION BB545848
VERSION BB545848.2 GI:16447378
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 659)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,

Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
JOURNAL Unpublished (2001)
COMMENT On Jul 31, 2000 this sequence version replaced gi:9617276.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
FEATURES Location/Qualifiers
source 1. .659
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="E130306O04"
/tissue_type="eyeball"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 0 day neonate eyeball"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
ORIGIN

Query Match 100.0%; Score 16; DB 2; Length 659;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAAGGCA 16
||||||||||||||||
Db 434 AAAGCCACCCAAGGCA 419

RESULT 10
CA083440
LOCUS CA083440 666 bp mRNA linear EST 23-SEP-2003
DEFINITION SCEPAM2013G09.g AM2 Saccharum officinarum cDNA clone SCEPAM2013G09 5', mRNA sequence.
ACCESSION CA083440
VERSION CA083440.1 GI:34936751
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.
REFERENCE 1 (bases 1 to 666)
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
Plate: 013 row: G column: 09
Seq primer: T7 Promoter Primer.
FEATURES Location/Qualifiers
source 1. .666
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCEPAM2013G09"
/lab_host="DH10B"
/clone_lib="AM2"
/note="Organ: Apical meristem and tissues surrounding of immature plants; Vector: pSport1; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from [Apical meristem and tissues surrounding of immature plants]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
ORIGIN

Query Match 100.0%; Score 16; DB 6; Length 666;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAAGGCA 16
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Db 471 AAAGCCACCCAAGGCA 486

RESULT 11
AV359761/c
LOCUS AV359761 700 bp mRNA linear EST 24-OCT-2001
DEFINITION AV359761 RIKEN full-length enriched, adult male eyeball Mus musculus cDNA clone 7530401G06 3', mRNA sequence.
ACCESSION AV359761

VERSION AV359761.2 GI:16397410
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 700)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
JOURNAL Unpublished (2001)
COMMENT On Nov 13, 1999 this sequence version replaced gi:6406899.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
FEATURES Location/Qualifiers
source 1. .700
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="7530401G06"
/sex="male"
/tissue_type="eyeball"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male eyeball"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"
ORIGIN

Query Match 100.0%; Score 16; DB 1; Length 700;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAAGGCA 16
||||||||||||||||
Db 110 AAAGCCACCCAAGGCA 95

RESULT 12
CD778583/c
LOCUS CD778583 770 bp mRNA linear EST 01-JUL-2004
DEFINITION EST649944 RAA Rhipicephalus appendiculatus cDNA clone RAAA309 3' end, mRNA sequence.
ACCESSION CD778583
VERSION CD778583.1 GI:49534256
KEYWORDS EST.
SOURCE Rhipicephalus appendiculatus
ORGANISM Rhipicephalus appendiculatus
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari; Parasitiformes; Ixodida; Ixodoidea; Ixodidae; Rhipicephalus.
REFERENCE 1 (bases 1 to 770)
AUTHORS Nene,V., Lee,Y., Skilton,R., Mwaura,S., Quackenbush,J., Gardner,M. and Bishop,R.
TITLE An index of genes transcribed in the salivary glands of Rhipicephalus appendiculatus
JOURNAL Unpublished (2003)
COMMENT Other_ESTs: EST649945
Contact: Vishvanath Nene
Parasite Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-610-5968
Fax: 301-838-0208
Email: nene@tigr.org
Seq primer: mixed oligo dT.
FEATURES Location/Qualifiers
source 1. .770
/organism="Rhipicephalus appendiculatus"
/mol_type="mRNA"
/strain="Muguga"
/db_xref="taxon:34631"
/clone="RAAA309"
/dev_stage="Adult"
/lab_host="E. coli strain DH10B-TonA"
/clone_lib="RAA"
/note="Organ: Salivary glands; Vector: pCMVSport6.0.ccdb; Salivary glands were dissected on day four after initiation of feeding. Total RNA was prepared using acid guanidium thiocyanate-phenol-chloroform extraction. The cDNA library was custom prepared by Invitrogen Corporation. Briefly, first strand cDNA was primed using oligo(dT) containing a NotI site. Size fractionated double stranded cDNA was ligated to EcoRV-NotI cleaved vector and electroporated into E.coli. Library RAA was made from uninfected ticks."
ORIGIN

Query Match 100.0%; Score 16; DB 6; Length 770;

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  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db        257 AAAGCCACCCAAGGCA 242


RESULT 13
BI250824
LOCUS       BI250824                 895 bp    mRNA    linear   EST 17-JUL-2001
DEFINITION  602993448F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5149306 5',
            mRNA sequence.
ACCESSION   BI250824
VERSION     BI250824.1  GI:14799568
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 895)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11368  row: p  column: 11
            High quality sequence start: 4
            High quality sequence stop: 741.
FEATURES             Location/Qualifiers
     source          1. .895
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="mix FVB/N, C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5149306"
                     /tissue_type="tumor, gross tissue"
                     /dev_stage="7 months"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Mam5"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigators
                     providing samples: Lothar Hennighausen/Robin Humphreys,
                     NIH"
ORIGIN

  Query Match             100.0%;  Score 16;  DB 4;  Length 895;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          2 AAAGCCACCCAAGGCA 17


RESULT 14
CA474404/c
LOCUS       CA474404                 975 bp    mRNA    linear   EST 12-NOV-2002
DEFINITION  AGENCOURT_10667749 NCI_CGAP_ZKid1 Danio rerio cDNA clone
            IMAGE:6795444 5', mRNA sequence.
ACCESSION   CA474404
VERSION     CA474404.1  GI:24930756
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 975)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Leonard I. Zon, M.D.
             cDNA Library Preparation: Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14305  row: i  column: 11
            High quality sequence stop: 314.
FEATURES             Location/Qualifiers
     source          1. .975
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:6795444"
                     /lab_host="DH10B (T1-resistant)"
                     /clone_lib="NCI_CGAP_ZKid1"
                     /note="Organ: kidney; Vector: pCMV-SPORT6.1; Site_1:
                     EcoRV; Site_2: NotI; Cloned unidirectionally. Primer:
                     Oligo dT. Average insert size 1.8 kb. Constructed by J.
                     Wang (Research Genetics, Invitrogen Corp) from tissue
                     donated by L. Zon (Harvard University). Note: this is a
                     NCI_CGAP Library."
ORIGIN

  Query Match             100.0%;  Score 16;  DB 6;  Length 975;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db        621 AAAGCCACCCAAGGCA 606


RESULT 15
W34362/c
LOCUS       W34362                   987 bp    mRNA    linear   EST 11-SEP-1996
DEFINITION  ma99b12.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone
            IMAGE:318815 5' similar to SW:KELC_DROME Q04652 RING CANAL PROTEIN
            ;, mRNA sequence.
ACCESSION   W34362
VERSION     W34362.1  GI:1316273
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
```

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           MGI:209431
           Seq primer: ETPrimer
           High quality sequence stop: 363.
FEATURES             Location/Qualifiers
     source          1. .987
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                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:318815"
                     /dev_stage="19.5 dpc total fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares mouse p3NMF19.5"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. RNA was kindly provided by
                     Dr. Minoru Ko (Wayne State University)."
ORIGIN

  Query Match             100.0%;  Score 16;  DB 7;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db        361 AAAGCCACCCAAGGCA 346


Search completed: March 29, 2005, 07:36:19
Job time : 2037 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 29, 2005, 07:40:19 ; Search time 1445 Seconds
(without alignments)
536.528 Million cell updates/sec

Title: US-09-888-164-29
Perfect score: 16
Sequence: 1 aaagccacccaaggca 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	16	100.0	16	6	A66874	A66874 Sequence 41
	2	16	100.0	16	6	I55199	I55199 Sequence 48
	3	16	100.0	16	6	AR271346	AR271346 Sequence
	4	16	100.0	16	6	AR488376	AR488376 Sequence
	5	16	100.0	18	6	A66882	A66882 Sequence 49
	6	16	100.0	18	6	I65373	I65373 Sequence 22
	7	16	100.0	18	6	AR488384	AR488384 Sequence
c	8	16	100.0	19	6	I65372	I65372 Sequence 21
c	9	16	100.0	19	6	I65376	I65376 Sequence 25
c	10	16	100.0	20	6	A18805	A18805 oligonucleo
c	11	16	100.0	20	6	A18806	A18806 oligonucleo
	12	16	100.0	20	6	AR086981	AR086981 Sequence
	13	16	100.0	20	6	E08672	E08672 PCR primer
	14	16	100.0	21	6	AR086970	AR086970 Sequence
	15	16	100.0	21	6	I55196	I55196 Sequence 45
	16	16	100.0	21	6	I55198	I55198 Sequence 47
	17	16	100.0	21	6	I92344	I92344 Sequence 5
	18	16	100.0	21	6	AR271343	AR271343 Sequence
	19	16	100.0	21	6	AR271345	AR271345 Sequence
c	20	16	100.0	23	6	A18804	A18804 oligonucleo
c	21	16	100.0	23	6	AR000182	AR000182 Sequence
c	22	16	100.0	23	6	E09725	E09725 Primer OAL4
c	23	16	100.0	23	6	AX250613	AX250613 Sequence
c	24	16	100.0	44	6	I65370	I65370 Sequence 19
c	25	16	100.0	44	6	I65371	I65371 Sequence 20
c	26	16	100.0	50	6	AR000194	AR000194 Sequence
	27	15	93.8	16	6	AR087000	AR087000 Sequence
	28	15	93.8	20	6	AR086982	AR086982 Sequence
c	29	15	93.8	30	6	BD141709	BD141709 Method fo
c	30	15	93.8	33	6	AX147027	AX147027 Sequence
	31	14.4	90.0	16	6	AR087003	AR087003 Sequence
	32	14.4	90.0	20	6	AX487887	AX487887 Sequence
	33	14	87.5	18	6	AR086991	AR086991 Sequence
	34	14	87.5	20	6	AR027815	AR027815 Sequence
c	35	14	87.5	30	6	A07794	A07794 Nucleotide
c	36	14	87.5	35	6	A00984	A00984 BamHI site
c	37	14	87.5	35	6	A01721	A01721 Expression
c	38	13.4	83.8	20	6	AX296496	AX296496 Sequence
c	39	13.4	83.8	24	6	AX291863	AX291863 Sequence
c	40	13.4	83.8	41	6	AX516081	AX516081 Sequence
c	41	13.4	83.8	41	6	AX517487	AX517487 Sequence
	42	13	81.2	16	6	I55201	I55201 Sequence 50
	43	13	81.2	16	6	AR271348	AR271348 Sequence
	44	13	81.2	20	6	AR000183	AR000183 Sequence
	45	13	81.2	21	6	I55200	I55200 Sequence 49

ALIGNMENTS

RESULT 1
A66874
LOCUS A66874 16 bp DNA linear PAT 29-MAR-1999
DEFINITION Sequence 41 from Patent WO9740193.
ACCESSION A66874
VERSION A66874.1 GI:4538245
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Stuyver,L., Rossau,R. and Maertens,G.
TITLE METHOD FOR TYPING AND DETECTING HBV
JOURNAL Patent: WO 9740193-A 41 30-OCT-1997;
INNOGENETICS NV (BE)
FEATURES Location/Qualifiers
source 1. .16
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN

Query Match 100.0%; Score 16; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAAGGCA 16
||||||||||||||||
Db 1 AAAGCCACCCAAGGCA 16

RESULT 2
I55199
LOCUS I55199 16 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 48 from patent US 5646262.
ACCESSION I55199
VERSION I55199.1 GI:2476402
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)

```
  AUTHORS   Korba,B.E. and Gerin,J.L.
  TITLE     Antisense oligonucleotides against hepatitis B viral replication
  JOURNAL   Patent: US 5646262-A 48 08-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .16
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ORIGIN

  Query Match            100.0%;  Score 16;  DB 6;  Length 16;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 3
AR271346
LOCUS       AR271346                  16 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 48 from patent US 6503533.
ACCESSION   AR271346
VERSION     AR271346.1  GI:29702721
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Korba,B.E. and Gerin,J.L.
  TITLE     Antisense ogligonucleotides against Hepatitis B viral replication
  JOURNAL   Patent: US 6503533-A 48 07-JAN-2003;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match            100.0%;  Score 16;  DB 6;  Length 16;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 4
AR488376
LOCUS       AR488376                  16 bp    DNA     linear   PAT 15-MAY-2004
DEFINITION  Sequence 41 from patent US 6709812.
ACCESSION   AR488376
VERSION     AR488376.1  GI:47254428
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Stuyver,L., Rossau,R. and Maertens,G.
  TITLE     Method for typing and detecting HBV
  JOURNAL   Patent: US 6709812-A 41 23-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 5
A66882
LOCUS       A66882                    18 bp    DNA     linear   PAT 29-MAR-1999
DEFINITION  Sequence 49 from Patent WO9740193.
ACCESSION   A66882
VERSION     A66882.1  GI:4538253
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Stuyver,L., Rossau,R. and Maertens,G.
  TITLE     METHOD FOR TYPING AND DETECTING HBV
  JOURNAL   Patent: WO 9740193-A 49 30-OCT-1997;
            INNOGENETICS NV (BE)
FEATURES             Location/Qualifiers
     source          1. .18
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match            100.0%;  Score 16;  DB 6;  Length 18;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 6
I65373
LOCUS       I65373                    18 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 22 from patent US 5667974.
ACCESSION   I65373
VERSION     I65373.1  GI:2481943
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Birkenmeyer,L. and Mushahwar,I.K.
  TITLE     Method for detecting nucleic acid sequences using competitive
            amplification
  JOURNAL   Patent: US 5667974-A 22 16-SEP-1997;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            100.0%;  Score 16;  DB 6;  Length 18;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 7
AR488384
LOCUS       AR488384                  18 bp    DNA     linear   PAT 15-MAY-2004
DEFINITION  Sequence 49 from patent US 6709812.
ACCESSION   AR488384
VERSION     AR488384.1  GI:47254436
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
```

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          Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Stuyver,L., Rossau,R. and Maertens,G.
  TITLE     Method for typing and detecting HBV
  JOURNAL   Patent: US 6709812-A 49 23-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           100.0%;  Score 16;  DB 6;  Length 18;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 8
I65372/c
LOCUS       I65372                   19 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 21 from patent US 5667974.
ACCESSION   I65372
VERSION     I65372.1  GI:2481942
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Birkenmeyer,L. and Mushahwar,I.K.
  TITLE     Method for detecting nucleic acid sequences using competitive
            amplification
  JOURNAL   Patent: US 5667974-A 21 16-SEP-1997;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           100.0%;  Score 16;  DB 6;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         18 AAAGCCACCCAAGGCA 3


RESULT 9
I65376/c
LOCUS       I65376                   19 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 25 from patent US 5667974.
ACCESSION   I65376
VERSION     I65376.1  GI:2481946
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Birkenmeyer,L. and Mushahwar,I.K.
  TITLE     Method for detecting nucleic acid sequences using competitive
            amplification
  JOURNAL   Patent: US 5667974-A 25 16-SEP-1997;
FEATURES             Location/Qualifiers
     source          1. .19
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ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         18 AAAGCCACCCAAGGCA 3


RESULT 10
A18805/c
LOCUS       A18805                   20 bp    DNA     linear   PAT 22-APR-1994
DEFINITION  oligonucleotide primer.
ACCESSION   A18805
VERSION     A18805.1  GI:513426
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   .
  TITLE     PROGNOSIS OF HEPATITIS INFECTION
  JOURNAL   Patent: WO 9114789-A 2 03-OCT-1991;
FEATURES             Location/Qualifiers
     source          1. .20
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                     /mol_type="unassigned DNA"
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ORIGIN

  Query Match           100.0%;  Score 16;  DB 6;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         19 AAAGCCACCCAAGGCA 4


RESULT 11
A18806/c
LOCUS       A18806                   20 bp    DNA     linear   PAT 22-APR-1994
DEFINITION  oligonucleotide primer.
ACCESSION   A18806
VERSION     A18806.1  GI:513427
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   .
  TITLE     PROGNOSIS OF HEPATITIS INFECTION
  JOURNAL   Patent: WO 9114789-A 3 03-OCT-1991;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match           100.0%;  Score 16;  DB 6;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         19 AAAGCCACCCAAGGCA 4


RESULT 12
AR086981
LOCUS       AR086981                 20 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 18 from patent US 5985662.
ACCESSION   AR086981
VERSION     AR086981.1  GI:10013747
```

```
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Anderson,K.P. and Cowsert,L.M.
  TITLE     Antisense inhibition of hepatitis B virus replication
  JOURNAL   Patent: US 5985662-A 18 16-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 16;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 13
E08672
LOCUS       E08672                     20 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  PCR primer for gaining polypeptide from X protein of Hepatitis B
            virus.
ACCESSION   E08672
VERSION     E08672.1  GI:2176785
KEYWORDS    JP 1995033797-A/5.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Uchida,T. and Shikata,T.
  TITLE     HEPATITIS B VIRUS-DERIVED POLYPEPTIDE AND GENE CODING THE SAME
            POLYPEPTIDE
  JOURNAL   Patent: JP 1995033797-A 5 03-FEB-1995;
            MITSUBISHI CHEM CORP
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1995033797-A/5
            PD   03-FEB-1995
            PF   21-JUL-1993 JP 1993180314
            PI   UCHIDA TOSHIKAZU, SHIKATA TOSHIO
            PC   C07K14/02,C12N15/09,C12P21/02,G01N33/53,G01N33/569,G01N33/576;
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .20
            FT                   /organism='Artificial sequences' FT
            misc_feature    1. .20
            FT                   /note='Primer p205'.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             100.0%;  Score 16;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          3 AAAGCCACCCAAGGCA 18


RESULT 14
AR086970
LOCUS       AR086970                   21 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 7 from patent US 5985662.
ACCESSION   AR086970
VERSION     AR086970.1  GI:10013736
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Anderson,K.P. and Cowsert,L.M.
  TITLE     Antisense inhibition of hepatitis B virus replication
  JOURNAL   Patent: US 5985662-A 7 16-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 16;  DB 6;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          3 AAAGCCACCCAAGGCA 18


RESULT 15
I55196
LOCUS       I55196                     21 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 45 from patent US 5646262.
ACCESSION   I55196
VERSION     I55196.1  GI:2476399
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Korba,B.E. and Gerin,J.L.
  TITLE     Antisense oligonucleotides against hepatitis B viral replication
  JOURNAL   Patent: US 5646262-A 45 08-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 16;  DB 6;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


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Job time : 1449 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 29, 2005, 07:38:14 ; Search time 261 Seconds
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Perfect score: 16
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Gapop 10.0 , Gapext 1.0

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Listing first 45 summaries

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13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	16	100.0	16	2	AAT18256	Aat18256 HBV epsil
	2	16	100.0	16	2	AAV14125	Aav14125 Probe HBP
	3	16	100.0	16	10	ADB68575	Adb68575 NG3 A-L-P
c	4	16	100.0	17	8	ACD55710	Acd55710 HBV amber
c	5	16	100.0	17	8	ACD53930	Acd53930 HBV zinzy
c	6	16	100.0	17	12	ADM59621	Adm59621 Hepatitis
c	7	16	100.0	17	12	ADM60244	Adm60244 Hepatitis
	8	16	100.0	18	2	AAT71786	Aat71786 Hepatitis
	9	16	100.0	18	2	AAV14133	Aav14133 Probe HBP
c	10	16	100.0	19	2	AAT71785	Aat71785 Hepatitis
c	11	16	100.0	19	2	AAT71789	Aat71789 Hepatitis
c	12	16	100.0	19	11	ADM00160	Adm00160 Hepatitis
	13	16	100.0	19	11	ADM00806	Adm00806 Hepatitis
	14	16	100.0	19	11	ADM00807	Adm00807 Hepatitis
	15	16	100.0	19	11	ADM00284	Adm00284 Hepatitis
	16	16	100.0	19	11	ADM00804	Adm00804 Hepatitis
c	17	16	100.0	19	11	ADL99637	Adl99637 Hepatitis
c	18	16	100.0	19	11	ADM00161	Adm00161 Hepatitis
c	19	16	100.0	19	11	ADM00158	Adm00158 Hepatitis
c	20	16	100.0	20	2	AAQ13771	Aaq13771 HBV prime
c	21	16	100.0	20	2	AAQ13772	Aaq13772 HBV prime
	22	16	100.0	20	2	AAQ85970	Aaq85970 Hepatitis
	23	16	100.0	20	2	AAT70947	Aat70947 HBV pre-g
	24	16	100.0	21	2	AAQ92909	Aaq92909 Antiviral
	25	16	100.0	21	2	AAT18255	Aat18255 HBV epsil
	26	16	100.0	21	2	AAT18253	Aat18253 HBV epsil
	27	16	100.0	21	2	AAT70936	Aat70936 HBV core
c	28	16	100.0	21	9	ADA13842	Ada13842 Short int
c	29	16	100.0	21	11	ADM00924	Adm00924 Hepatitis
c	30	16	100.0	23	2	AAQ13770	Aaq13770 HBV prime
c	31	16	100.0	23	2	AAT03266	Aat03266 Hepatitis
c	32	16	100.0	23	2	AAQ81424	Aaq81424 HBV hybri
c	33	16	100.0	23	4	AAD19005	Aad19005 Hepatitis
c	34	16	100.0	23	11	ADM00880	Adm00880 Hepatitis
c	35	16	100.0	30	2	AAV29303	Aav29303 Hepatitis
c	36	16	100.0	32	4	AAS14628	Aas14628 NASBA mol
c	37	16	100.0	44	2	AAT71784	Aat71784 Hepatitis
c	38	16	100.0	44	2	AAT71783	Aat71783 Hepatitis
c	39	16	100.0	48	3	ABK14698	Abk14698 HBV encap
c	40	16	100.0	48	3	ABK14696	Abk14696 RNA targe
c	41	16	100.0	50	2	AAQ81436	Aaq81436 HBV targe
	42	15	93.8	16	2	AAT70966	Aat70966 HBV pre-g
c	43	15	93.8	17	8	ACD55709	Acd55709 HBV amber
c	44	15	93.8	17	12	ADM60243	Adm60243 Hepatitis
c	45	15	93.8	19	11	ADL99647	Adl99647 Hepatitis

ALIGNMENTS

RESULT 1
AAT18256
ID AAT18256 standard; DNA; 16 BP.
XX
AC AAT18256;
XX
DT 17-SEP-1996 (first entry)
XX
DE HBV epsilon encapsidation mRNA intermediate antisense oligo L2c.
XX
KW Inhibition; replication; hepatitis B virus; HBV; antisense; mRNA;
KW epsilon; encapsidation; sequence; intermediate; subtype ayw; C gene;
KW treatment; chronic infection; modulation; translation; transcription;
KW release; host cell; ss.
XX
OS Synthetic.
XX
PN WO9603152-A1.
XX
PD 08-FEB-1996.
XX
PF 28-JUL-1995; 95WO-US009143.
XX
PR 28-JUL-1994; 94US-00281106.
XX
PA (GEOU) UNIV GEORGETOWN.
XX
PI Korba BE, Gerin JL;
XX
DR WPI; 1996-116796/12.
XX
PT Single stranded oligo:nucleotide(s) for inhibiting replication of
PT hepatitis B virus - are anti-sense to portions of the epsilon
PT encapsidation sequence and modulate HBV function.
XX
PS Claim 15; Page 44; 56pp; English.
XX
CC The present sequence, which inhibits the replication of hepatitis B virus
CC (HBV) in a host cell, is a single stranded antisense oligonucleotide that
CC binds the epsilon encapsidation sequence of a mRNA intermediate derived
CC from the HBV genome. The 1st nucleotide of the oligonucleotide
CC corresponds to nucleotide 1884 of the HBV ayw subtype C gene, using the
CC numbering scheme from the sequence published by Galibert et al., Nature

CC 281: 646 (1979). A compsn. comprising the oligonucleotide may be used to
CC treat chronic HBV infection by modulating a HBV related function, e.g.
CC translation, transcription, encapsidation, replication and release from a
CC host cell. The effect of the oligonucleotide on the levels of HBV DNA in
CC the extracellular medium (VIR. DNA), intracellular viral replicative
CC intermediates (HBV RI), intracellular viral RNA (HBV RNA), HBV surface
CC antigen protein (HBsAg), HBV e antigen protein (HBeAg) and HBV core
CC antigen protein (HBcAg), given as the EC(90) (microM, 9 days of
CC treatment) or ND (not determined), are VIR. DNA (1.6), HBV RI (5.1), HBV
CC RNA (>20), HBsAg (>20), HBeAg (>20) and HBcAg (18.5)
XX
SQ Sequence 16 BP; 7 A; 6 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAAGGCA 16
||||||||||||||||
Db 1 AAAGCCACCCAAGGCA 16

RESULT 2
AAV14125
ID AAV14125 standard; DNA; 16 BP.
XX
AC AAV14125;
XX
DT 27-AUG-2003 (revised)
DT 19-MAY-1998 (first entry)
XX
DE Probe HBPr41 for preCore region of HBV.
XX
KW Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis;
KW preCore region; HBsAg region; genotype specific target;
KW mutation detection; ss.
XX
OS Synthetic.
OS Hepatitis B virus.
XX
PN WO9740193-A2.
XX
PD 30-OCT-1997.
XX
PF 21-APR-1997; 97WO-EP002002.
XX
PR 19-APR-1996; 96EP-00870053.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Stuyver L, Rossau R, Maertens G;
XX
DR WPI; 1997-535867/49.
XX
PT Detection and/or genetic analysis of hepatitis B virus - specifically
PT genotype, preCore mutations, vaccine escape mutations and RT gene
PT mutations selected by treatment with drugs.
XX
PS Claim 5; Page 27; 80pp; English.
XX
CC This sequence represents a probe for the preCore region of hepatitis b
CC virus (HBV). This sequence can be used in the method of the invention for
CC detection and/or genetic analysis of hepatitis B virus (HBV) in a sample.
CC The method comprises: (a) optionally releasing, isolating or
CC concentrating polynucleic acids (I) in the sample, and amplifying the
CC relevant part of a suitable HBV gene in the sample with at least 1
CC suitable primer pair; (b) hybridising (I) with a combination of at least
CC 2 nucleotide probes, which are applied to known locations on a solid
CC support and hybridise specifically to mutant target sequences chosen from
CC the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
CC genotype specific target sequences, or their complements or U for T
CC homologues; (c) detecting the hybrids formed in step (b), and inferring
CC the HBV genotype and/or mutants present in the sample from the
CC differential hybridisation signal(s). The composition can be used to
CC diagnose and/or monitor HBV mutants and/or genotypes in a sample,
CC specifically genotype, preCore mutations, vaccine escape mutations and RT
CC gene mutations selected by treatment with drugs, e.g. lamivudune and
CC penciclovir. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 16 BP; 7 A; 6 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAAGGCA 16
||||||||||||||||
Db 1 AAAGCCACCCAAGGCA 16

RESULT 3
ADB68575
ID ADB68575 standard; DNA; 16 BP.
XX
AC ADB68575;
XX
DT 04-DEC-2003 (first entry)
XX
DE NG3 A-L-P conjugate DNA component used to target HBV e-site.
XX
KW homogeneous A-L-P conjugate; hepatic; chronic viral hepatitis; cirrhosis;
KW malaria; viral infection; protozoan; cancer; hepatocellular carcinoma;
KW HCC; ss; NG3; HBV; e-site; pregenome.
XX
OS Hepatitis B virus.
XX
FH Key Location/Qualifiers
FT modified_base 1. .16
FT /*tag= b
FT /mod_base= OTHER
FT /note= "OTHER = phosphorothioate backbone"
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER = Optionally linked to YEE(ahGalNAc)3-SMCC
FT and various chemical groups as shown in figures"
FT modified_base 16
FT /*tag= c
FT /mod_base= OTHER
FT /note= "OTHER = Optionally linked to chemical group as
FT shown in figure 5"
XX
PN WO2003067209-A2.
XX
PD 14-AUG-2003.
XX
PF 21-JUN-2002; 2002WO-US019908.
XX
PR 22-JUN-2001; 2001US-00888164.
XX
PA (CELL-) CELL WORKS INC.
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Ts'o POP, Duff R, Zhou Y, Deamond S, Roby C;
XX
DR WPI; 2003-697456/66.
XX
PT New homogeneous prodrug conjugate containing hepatic ligand for delivery
PT of pathogen-specific oligomer useful for treating liver infections or
PT cancer.
XX
PS Claim 7; Page 83; 107pp; English.
XX
CC The invention relates to a novel homogeneous conjugate comprising a
CC hepatic ligand, bifunctional linker and biologically stable oligomer that
CC binds to a sequence in a hepatic virus or pathogen and is released from

```
CC   the conjugate by hydrolysis or reduction. The conjugate of the invention
CC   may be useful during the treatment of liver diseases including chronic
CC   viral hepatitis, cirrhosis, malaria, viral or protozoan infection and
CC   cancer, such as hepatocellular carcinoma (HCC). The current sequence is
CC   that of the NG3 A-L-P conjugate DNA component of the invention which was
CC   used to target the Hepatitis B virus (HBV) pregenome (e-site).
XX
SQ   Sequence 16 BP; 7 A; 6 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 16;  DB 10;  Length 16;
  Best Local Similarity  100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 4
ACD55710/c
ID   ACD55710 standard; RNA; 17 BP.
XX
AC   ACD55710;
XX
DT   23-SEP-2003  (first entry)
XX
DE   HBV amberzyme substrate sequence #183.
XX
KW   Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW   RNA stability; RNA expression; RNA synthesis; antisense;
KW   enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW   amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW   HBV reverse transcriptase; Enhancer I region; viral replication;
KW   degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW   liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW   virucide; antiinflammatory; substrate; ss.
XX
OS   Hepatitis B virus.
XX
PN   WO200281494-A1.
XX
PD   17-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009187.
XX
PR   26-MAR-2001; 2001US-00817879.
PR   08-JUN-2001; 2001US-00877478.
PR   08-JUN-2001; 2001US-0296876P.
PR   24-OCT-2001; 2001US-0335059P.
PR   05-DEC-2001; 2001US-0337055P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MACE/) MACEJAK D.
PA   (MCSW/) MCSWIGGEN J.
PA   (MORR/) MORRISSEY D.
PA   (PAVC/) PAVCO P.
PA   (LEEP/) LEE P.
PA   (DRAP/) DRAPER K.
PA   (ROBE/) ROBERTS E.
XX
PI   Blatt L,  Macejak D,  Mcswiggen J,  Morrissey D,  Pavco P,  Lee P;
PI   Draper K,  Roberts E;
XX
DR   WPI; 2003-229207/22.
XX
PT   Novel compound useful for treating cirrhosis, liver failure,
PT   hepatocellular carcinoma, or condition associated with hepatitis C virus
PT   infection.
XX
PS   Example 1; Page 207; 387pp; English.
XX
CC   The present invention relates to nucleic acid molecules which modulate
CC   the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC   Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC   and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
CC   inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC   are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC   transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC   as oligonucleotides that specifically bind the Enhancer I region of HBV
CC   DNA. The nucleic acids may be used to modulate the expression of HBV
CC   genes and HBV viral replication. Also disclosed is a method for screening
CC   compounds and/or potential therapies directed against HBV, and compounds
CC   that modulate the expression and/or replication of HCV. The compounds and
CC   methods of the invention are useful for the treatment of degenerative and
CC   disease states related to HBV and HCV infection, replication and gene
CC   expression such as cirrhosis, liver failure, and hepatocellular
CC   carcinoma. The present sequence represents a substrate for one of the HBV
CC   ribozyme, inozyme, G-cleaver, zinzyme, DNAzyme or amberzyme sequences
CC   disclosed in the present invention
XX
SQ   Sequence 17 BP; 0 A; 3 C; 7 G; 0 T; 7 U; 0 Other;

  Query Match            100.0%;  Score 16;  DB 8;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         17 AAAGCCACCCAAGGCA 2


RESULT 5
ACD53930/c
ID   ACD53930 standard; RNA; 17 BP.
XX
AC   ACD53930;
XX
DT   24-SEP-2003  (first entry)
XX
DE   HBV zinzyme substrate sequence #100.
XX
KW   Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW   RNA stability; RNA expression; RNA synthesis; antisense;
KW   enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW   amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW   HBV reverse transcriptase; Enhancer I region; viral replication;
KW   degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW   liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW   virucide; antiinflammatory; substrate; ss.
XX
OS   Hepatitis B virus.
XX
PN   WO200281494-A1.
XX
PD   17-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009187.
XX
PR   26-MAR-2001; 2001US-00817879.
PR   08-JUN-2001; 2001US-00877478.
PR   08-JUN-2001; 2001US-0296876P.
PR   24-OCT-2001; 2001US-0335059P.
PR   05-DEC-2001; 2001US-0337055P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MACE/) MACEJAK D.
PA   (MCSW/) MCSWIGGEN J.
PA   (MORR/) MORRISSEY D.
PA   (PAVC/) PAVCO P.
PA   (LEEP/) LEE P.
PA   (DRAP/) DRAPER K.
PA   (ROBE/) ROBERTS E.
XX
PI   Blatt L,  Macejak D,  Mcswiggen J,  Morrissey D,  Pavco P,  Lee P;
```

PI Draper K, Roberts E;
XX
DR WPI; 2003-229207/22.
XX
PT Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
PS Example 1; Page 175; 387pp; English.
XX
CC The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HBV
CC ribozyme, inozyme, G-cleaver, zinzyme, DNAzyme or amberzyme sequences
CC disclosed in the present invention
XX
SQ Sequence 17 BP; 0 A; 3 C; 7 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 16; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAAGGCA 16
||||||||||||||||
Db 16 AAAGCCACCCAAGGCA 1

RESULT 6
ADM59621/c
ID ADM59621 standard; RNA; 17 BP.
XX
AC ADM59621;
XX
DT 03-JUN-2004 (first entry)
XX
DE Hepatitis B virus (HBV) RNA target sequence #1755.
XX
KW Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;
KW hepatitis B virus infection; hepatitis; hepatocellular carcinoma;
KW cirrhosis; liver failure; lamivudine; interferon; genetic drift;
KW virucide; hepatotropic; antiinflammatory; cytostatic.
XX
OS Hepatitis B virus.
XX
PN US2004054156-A1.
XX
PD 18-MAR-2004.
XX
PF 15-JAN-2003; 2003US-00342902.
XX
PR 14-MAY-1992; 92US-00882712.
PR 07-FEB-1994; 94US-00193627.
PR 08-NOV-1999; 99US-00436430.
PR 20-MAR-2000; 2000US-00531025.
PR 09-AUG-2000; 2000US-00636385.
PR 24-OCT-2000; 2000US-00696347.
PR 08-JUN-2001; 2001US-00877478.
XX
PA (DRAP/) DRAPER K.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (MORR/) MORRISSEY D.
XX
PI Draper K, Blatt L, Mcswiggen JA, Morrissey D;
XX
DR WPI; 2004-247781/23.
XX
PT Novel enzymatic nucleic acid molecule such as DNAzymes and inozymes
PT specifically cleaving RNA derived from hepatitis B virus and comprising
PT one or more binding arms, useful for treating hepatitis and cirrhosis.
XX
PS Disclosure; SEQ ID NO 1755; 122pp; English.
XX
CC The invention relates to an enzymatic nucleic acid molecule that
CC specifically cleaves RNA derived from hepatitis B virus (HBV) and
CC comprising one or more binding arms, without requiring the presence of a
CC 2'-OH group within the molecule for activity. The nucleic acids are
CC useful for treating hepatitis B virus infection, hepatitis,
CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in
CC combination with other therapies such as lamivudine and interferons. The
CC nucleic acids are useful as diagnostic tools to examine genetic drift and
CC mutations within diseased cells, for detecting the presence of HBV RNA in
CC a cell, for the study of RNA and for down-regulating gene expression of
CC target genes in bacterial, fungal, viral, plant or mammalian cells. This
CC sequence represents an HBV RNA target sequence, used in the scope of the
CC invention. Note: The sequence data for this patent is also available in
CC electronic format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 17 BP; 0 A; 3 C; 7 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 16; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAAGGCA 16
||||||||||||||||
Db 16 AAAGCCACCCAAGGCA 1

RESULT 7
ADM60244/c
ID ADM60244 standard; RNA; 17 BP.
XX
AC ADM60244;
XX
DT 03-JUN-2004 (first entry)
XX
DE Hepatitis B virus (HBV) RNA target sequence #2378.
XX
KW Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;
KW hepatitis B virus infection; hepatitis; hepatocellular carcinoma;
KW cirrhosis; liver failure; lamivudine; interferon; genetic drift;
KW virucide; hepatotropic; antiinflammatory; cytostatic.
XX
OS Hepatitis B virus.
XX
PN US2004054156-A1.
XX
PD 18-MAR-2004.
XX
PF 15-JAN-2003; 2003US-00342902.
XX
PR 14-MAY-1992; 92US-00882712.
PR 07-FEB-1994; 94US-00193627.
PR 08-NOV-1999; 99US-00436430.
PR 20-MAR-2000; 2000US-00531025.
PR 09-AUG-2000; 2000US-00636385.
PR 24-OCT-2000; 2000US-00696347.
PR 08-JUN-2001; 2001US-00877478.
XX
PA (DRAP/) DRAPER K.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.

```
PA   (MORR/) MORRISSEY D.
XX
PI   Draper K,  Blatt L,  Mcswiggen JA,  Morrissey D;
XX
DR   WPI; 2004-247781/23.
XX
PT   Novel enzymatic nucleic acid molecule such as DNAzymes and inozymes
PT   specifically cleaving RNA derived from hepatitis B virus and comprising
PT   one or more binding arms, useful for treating hepatitis and cirrhosis.
XX
PS   Disclosure; SEQ ID NO 2378; 122pp; English.
XX
CC   The invention relates to an enzymatic nucleic acid molecule that
CC   specifically cleaves RNA derived from hepatitis B virus (HBV) and
CC   comprising one or more binding arms, without requiring the presence of a
CC   2'-OH group within the molecule for activity. The nucleic acids are
CC   useful for treating hepatitis B virus infection, hepatitis,
CC   hepatocellular carcinoma, cirrhosis and liver failure, either alone or in
CC   combination with other therapies such as lamivudine and interferons. The
CC   nucleic acids are useful as diagnostic tools to examine genetic drift and
CC   mutations within diseased cells, for detecting the presence of HBV RNA in
CC   a cell, for the study of RNA and for down-regulating gene expression of
CC   target genes in bacterial, fungal, viral, plant or mammalian cells. This
CC   sequence represents an HBV RNA target sequence, used in the scope of the
CC   invention. Note: The sequence data for this patent is also available in
CC   electronic format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ   Sequence 17 BP; 0 A; 3 C; 7 G; 0 T; 7 U; 0 Other;

  Query Match             100.0%;  Score 16;  DB 12;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         17 AAAGCCACCCAAGGCA 2


RESULT 8
AAT71786
ID   AAT71786 standard; DNA; 18 BP.
XX
AC   AAT71786;
XX
DT   29-AUG-1997  (first entry)
XX
DE   Hepatitis B virus precore antigen wild-type target sequence primer.
XX
KW   HBV; ligase chain reaction; internal standard; amplification; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1
FT                   /*tag=  a
FT                   /note= "Phosphorylated"
FT   misc_difference 18
FT                   /*tag=  b
FT                   /note= "Haptenated with fluoroscein"
XX
PN   WO9640996-A1.
XX
PD   19-DEC-1996.
XX
PF   03-JUN-1996;   96WO-US008429.
XX
PR   07-JUN-1995;   95US-00480220.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Birkenmeyer L,  Mushahwar IK;
XX
DR   WPI; 1997-052367/05.
XX
PT   Quantitative detection of target nucleic acid sequence, esp. hepatitis B
PT   virus - can distinguish wild-type and mutant DNA types.
XX
PS   Claim 14; Page 29; 40pp; English.
XX
CC   A novel method has been produced for detecting the amount of a target
CC   nucleic acid sequence which may be present in a test sample. It involves
CC   contacting the test sample with means for performing a nucleic acid
CC   amplification reaction; and determining the ratio of target amplification
CC   products to internal standard amplification products present in the
CC   sample. The present sequence represents a primer/target specific probe
CC   for the hepatitis B virus (HBV) precore antigen wild-type target sequence
CC   (AAT71783). The method can be used for distinguishing between two
CC   different nucleic acid sequences present in a sample e.g. wild-type and
CC   mutant. The compositions can be used for quantitatively detecting the DNA
CC   of HBV
XX
SQ   Sequence 18 BP; 8 A; 7 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 16;  DB 2;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 9
AAV14133
ID   AAV14133 standard; DNA; 18 BP.
XX
AC   AAV14133;
XX
DT   27-AUG-2003  (revised)
DT   19-MAY-1998  (first entry)
XX
DE   Probe HBPr49 for preCore region of HBV.
XX
KW   Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis;
KW   preCore region; HBsAg region; genotype specific target;
KW   mutation detection; ss.
XX
OS   Synthetic.
OS   Hepatitis B virus.
XX
PN   WO9740193-A2.
XX
PD   30-OCT-1997.
XX
PF   21-APR-1997;   97WO-EP002002.
XX
PR   19-APR-1996;   96EP-00870053.
XX
PA   (INNO-) INNOGENETICS NV.
XX
PI   Stuyver L,  Rossau R,  Maertens G;
XX
DR   WPI; 1997-535867/49.
XX
PT   Detection and/or genetic analysis of hepatitis B virus - specifically
PT   genotype, preCore mutations, vaccine escape mutations and RT gene
PT   mutations selected by treatment with drugs.
XX
PS   Claim 5; Page 27; 80pp; English.
XX
CC   This sequence represents a probe for the preCore region of hepatitis b
CC   virus (HBV). This sequence can be used in the method of the invention for
CC   detection and/or genetic analysis of hepatitis B virus (HBV) in a sample.
CC   The method comprises: (a) optionally releasing, isolating or
CC   concentrating polynucleic acids (I) in the sample, and amplifying the
CC   relevant part of a suitable HBV gene in the sample with at least 1
```

```
CC   suitable primer pair; (b) hybridising (I) with a combination of at least
CC   2 nucleotide probes, which are applied to known locations on a solid
CC   support and hybridise specifically to mutant target sequences chosen from
CC   the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
CC   genotype specific target sequences, or their complements or U for T
CC   homologues; (c) detecting the hybrids formed in step (b), and inferring
CC   the HBV genotype and/or mutants present in the sample from the
CC   differential hybridisation signal(s). The composition can be used to
CC   diagnose and/or monitor HBV mutants and/or genotypes in a sample,
CC   specifically genotype, preCore mutations, vaccine escape mutations and RT
CC   gene mutations selected by treatment with drugs, e.g. lamivudune and
CC   penciclovir. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ   Sequence 18 BP; 8 A; 7 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 16;  DB 2;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 10
AAT71785/c
ID   AAT71785 standard; DNA; 19 BP.
XX
AC   AAT71785;
XX
DT   29-AUG-1997  (first entry)
XX
DE   Hepatitis B virus precore antigen wild-type target sequence primer.
XX
KW   HBV; ligase chain reaction; internal standard; amplification; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1
FT                   /*tag=  a
FT                   /note= "Haptenated with fluoroscein"
XX
PN   WO9640996-A1.
XX
PD   19-DEC-1996.
XX
PF   03-JUN-1996;   96WO-US008429.
XX
PR   07-JUN-1995;   95US-00480220.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Birkenmeyer L,  Mushahwar IK;
XX
DR   WPI; 1997-052367/05.
XX
PT   Quantitative detection of target nucleic acid sequence, esp. hepatitis B
PT   virus - can distinguish wild-type and mutant DNA types.
XX
PS   Claim 14; Page 29; 40pp; English.
XX
CC   A novel method has been produced for detecting the amount of a target
CC   nucleic acid sequence which may be present in a test sample. It involves
CC   contacting the test sample with means for performing a nucleic acid
CC   amplification reaction; and determining the ratio of target amplification
CC   products to internal standard amplification products present in the
CC   sample. The present sequence represents a primer/target specific probe
CC   for the hepatitis B virus (HBV) precore antigen wild-type target sequence
CC   (AAT71783). The method can be used for distinguishing between two
CC   different nucleic acid sequences present in a sample e.g. wild-type and
CC   mutant. The compositions can be used for quantitatively detecting the DNA
CC   of HBV
XX
SQ   Sequence 19 BP; 0 A; 3 C; 8 G; 8 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 16;  DB 2;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         18 AAAGCCACCCAAGGCA 3


RESULT 11
AAT71789/c
ID   AAT71789 standard; DNA; 19 BP.
XX
AC   AAT71789;
XX
DT   29-AUG-1997  (first entry)
XX
DE   Hepatitis B virus precore antigen mutant target sequence primer.
XX
KW   HBV; ligase chain reaction; internal standard; amplification; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1
FT                   /*tag=  a
FT                   /note= "Haptenated with fluorescein"
XX
PN   WO9640996-A1.
XX
PD   19-DEC-1996.
XX
PF   03-JUN-1996;   96WO-US008429.
XX
PR   07-JUN-1995;   95US-00480220.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Birkenmeyer L,  Mushahwar IK;
XX
DR   WPI; 1997-052367/05.
XX
PT   Quantitative detection of target nucleic acid sequence, esp. hepatitis B
PT   virus - can distinguish wild-type and mutant DNA types.
XX
PS   Claim 14; Page 30; 40pp; English.
XX
CC   A novel method has been produced for detecting the amount of a target
CC   nucleic acid sequence which may be present in a test sample. It involves
CC   contacting the test sample with means for performing a nucleic acid
CC   amplification reaction; and determining the ratio of target amplification
CC   products to internal standard amplification products present in the
CC   sample. The present sequence represents a primer/target specific probe
CC   for the hepatitis B virus (HBV) precore antigen mutant target sequence
CC   (AAT71784). The method can be used for distinguishing between two
CC   different nucleic acid sequences present in a sample e.g. wild-type and
CC   mutant. The compositions can be used for quantitatively detecting the DNA
CC   of HBV
XX
SQ   Sequence 19 BP; 1 A; 3 C; 7 G; 8 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 16;  DB 2;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         18 AAAGCCACCCAAGGCA 3
```

```
RESULT 12
ADM00160/c
ID   ADM00160 standard; RNA; 19 BP.
XX
AC   ADM00160;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Hepatitis B virus short interfering nucleic acid (siNA) #576.
XX
KW   Virucide; Hepatotropic; Gene therapy; ss; short interfering nucleic acid;
KW   siNA; hepatitis B virus; HBV; RNA interference.
XX
OS   Hepatitis B virus.
XX
PN   US2003206887-A1.
XX
PD   06-NOV-2003.
XX
PF   16-SEP-2002; 2002US-00244647.
XX
PR   14-MAY-1992;   92US-00882712.
PR   07-FEB-1994;   94US-00193627.
PR   08-NOV-1999;   99US-00436430.
PR   20-MAR-2000; 2000US-00531025.
PR   09-AUG-2000; 2000US-00636385.
PR   24-OCT-2000; 2000US-00696347.
PR   08-JUN-2001; 2001US-00877478.
PR   08-JUN-2001; 2001US-0296876P.
PR   24-OCT-2001; 2001US-0335059P.
PR   05-DEC-2001; 2001US-0337055P.
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   26-MAR-2002; 2002WO-US009187.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
XX
PA   (MORR/) MORRISSEY D.
PA   (MCSW/) MCSWIGGEN J A.
PA   (BEIG/) BEIGELMAN L.
XX
PI   Morrissey D,  Mcswiggen JA,  Beigelman L;
XX
DR   WPI; 2003-901032/82.
XX
PT   New short interfering nucleic acid molecules which down-regulates
PT   expression of a hepatitis B virus (HBV) or which inhibits HBV
PT   replication, useful for treating human HBV infections or for
PT   characterizing gene function.
XX
PS   Claim 11; Page 48; 72pp; English.
XX
CC   The invention relates to a short interfering nucleic acid (siNA) molecule
CC   that down-regulates expression of a hepatitis B virus (HBV) gene by RNA
CC   interference or that inhibits HBV replication. Also disclosed are the
CC   following: (i) a method of modulating the expression of a HBV gene in a
CC   tissue explant; (ii)) a method of generating a library of siNA constructs
CC   having predetermined complexity; (iii) a cell containing one or more siNA
CC   molecules; (iv)a kit containing a siNA molecule which can be used to
CC   modulate the expression of a HBV target gene in a cell, tissue or
CC   organism; and (v) a method for synthesising a siNA molecule. The siNA
CC   molecule is adapted for use to treat HBV infection, and comprises a sense
CC   and an antisense region, where the antisense region comprises sequence
CC   complementary to an RNA sequence encoding HBV and the sense region
CC   comprises sequence complementary to the antisense region. The siNA
CC   molecule is assembled from 2 nucleic acid fragments, where one fragment
CC   comprises the sense region and the second fragment comprises the
CC   antisense region of the siNA molecule, where sense region and the
CC   antisense region comprise separate oligonucleotides, and are covalently
CC   connected via a linker molecule. The linker molecule is a polynucleotide
CC   linker or a non-nucleotide linker. The sense region comprises a 3'-
CC   terminal overhang and the antisense region comprises a 3'-terminal
CC   overhang. The 3'-terminal overhangs each comprise about 2 nucleotides.
CC   The antisense region 3'-terminal overhang is complementary to RNA
CC   encoding HBV. The siNA is useful for treating human hepatitis B virus
CC   infections, and for characterising pathways of gene function, e.g. to
CC   inhibit activity of target genes in a pathway to determine the function
CC   of uncharacterised genes in gene function analysis. The siNA molecules
CC   may also be used in clinical, industrial, environmental, agricultural
CC   and/or research settings. The present sequence represents 1 of 1504 HBV
CC   siNA molecules of the invention.
XX
SQ   Sequence 19 BP; 0 A; 3 C; 9 G; 0 T; 7 U; 0 Other;

  Query Match             100.0%;  Score 16;  DB 11;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
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Db         16 AAAGCCACCCAAGGCA 1


RESULT 13
ADM00806
ID   ADM00806 standard; RNA; 19 BP.
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AC   ADM00806;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Hepatitis B virus short interfering nucleic acid (siNA) #1222.
XX
KW   Virucide; Hepatotropic; Gene therapy; ss; short interfering nucleic acid;
KW   siNA; hepatitis B virus; HBV; RNA interference.
XX
OS   Hepatitis B virus.
XX
PN   US2003206887-A1.
XX
PD   06-NOV-2003.
XX
PF   16-SEP-2002; 2002US-00244647.
XX
PR   14-MAY-1992;   92US-00882712.
PR   07-FEB-1994;   94US-00193627.
PR   08-NOV-1999;   99US-00436430.
PR   20-MAR-2000; 2000US-00531025.
PR   09-AUG-2000; 2000US-00636385.
PR   24-OCT-2000; 2000US-00696347.
PR   08-JUN-2001; 2001US-00877478.
PR   08-JUN-2001; 2001US-0296876P.
PR   24-OCT-2001; 2001US-0335059P.
PR   05-DEC-2001; 2001US-0337055P.
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   26-MAR-2002; 2002WO-US009187.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
XX
PA   (MORR/) MORRISSEY D.
PA   (MCSW/) MCSWIGGEN J A.
PA   (BEIG/) BEIGELMAN L.
XX
PI   Morrissey D,  Mcswiggen JA,  Beigelman L;
XX
DR   WPI; 2003-901032/82.
XX
PT   New short interfering nucleic acid molecules which down-regulates
PT   expression of a hepatitis B virus (HBV) or which inhibits HBV
PT   replication, useful for treating human HBV infections or for
PT   characterizing gene function.
```

XX
PS Claim 11; Page 48; 72pp; English.
XX
CC The invention relates to a short interfering nucleic acid (siNA) molecule
CC that down-regulates expression of a hepatitis B virus (HBV) gene by RNA
CC interference or that inhibits HBV replication. Also disclosed are the
CC following: (i) a method of modulating the expression of a HBV gene in a
CC tissue explant; (ii)) a method of generating a library of siNA constructs
CC having predetermined complexity; (iii) a cell containing one or more siNA
CC molecules; (iv)a kit containing a siNA molecule which can be used to
CC modulate the expression of a HBV target gene in a cell, tissue or
CC organism; and (v) a method for synthesising a siNA molecule. The siNA
CC molecule is adapted for use to treat HBV infection, and comprises a sense
CC and an antisense region, where the antisense region comprises sequence
CC complementary to an RNA sequence encoding HBV and the sense region
CC comprises sequence complementary to the antisense region. The siNA
CC molecule is assembled from 2 nucleic acid fragments, where one fragment
CC comprises the sense region and the second fragment comprises the
CC antisense region of the siNA molecule, where sense region and the
CC antisense region comprise separate oligonucleotides, and are covalently
CC connected via a linker molecule. The linker molecule is a polynucleotide
CC linker or a non-nucleotide linker. The sense region comprises a 3'-
CC terminal overhang and the antisense region comprises a 3'-terminal
CC overhang. The 3'-terminal overhangs each comprise about 2 nucleotides.
CC The antisense region 3'-terminal overhang is complementary to RNA
CC encoding HBV. The siNA is useful for treating human hepatitis B virus
CC infections, and for characterising pathways of gene function, e.g. to
CC inhibit activity of target genes in a pathway to determine the function
CC of uncharacterised genes in gene function analysis. The siNA molecules
CC may also be used in clinical, industrial, environmental, agricultural
CC and/or research settings. The present sequence represents 1 of 1504 HBV
CC siNA molecules of the invention.
XX
SQ Sequence 19 BP; 7 A; 9 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 4 AAAGCCACCCAAGGCA 19

RESULT 14
ADM00807
ID ADM00807 standard; RNA; 19 BP.
XX
AC ADM00807;
XX
DT 20-MAY-2004 (first entry)
XX
DE Hepatitis B virus short interfering nucleic acid (siNA) #1223.
XX
KW Virucide; Hepatotropic; Gene therapy; ss; short interfering nucleic acid;
KW siNA; hepatitis B virus; HBV; RNA interference.
XX
OS Hepatitis B virus.
XX
PN US2003206887-A1.
XX
PD 06-NOV-2003.
XX
PF 16-SEP-2002; 2002US-00244647.
XX
PR 14-MAY-1992; 92US-00882712.
PR 07-FEB-1994; 94US-00193627.
PR 08-NOV-1999; 99US-00436430.
PR 20-MAR-2000; 2000US-00531025.
PR 09-AUG-2000; 2000US-00636385.
PR 24-OCT-2000; 2000US-00696347.
PR 08-JUN-2001; 2001US-00877478.
PR 08-JUN-2001; 2001US-0296876P.
PR 24-OCT-2001; 2001US-0335059P.
PR 05-DEC-2001; 2001US-0337055P.
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
XX
PA (MORR/) MORRISSEY D.
PA (MCSW/) MCSWIGGEN J A.
PA (BEIG/) BEIGELMAN L.
XX
PI Morrissey D, Mcswiggen JA, Beigelman L;
XX
DR WPI; 2003-901032/82.
XX
PT New short interfering nucleic acid molecules which down-regulates
PT expression of a hepatitis B virus (HBV) or which inhibits HBV
PT replication, useful for treating human HBV infections or for
PT characterizing gene function.
XX
PS Claim 11; Page 48; 72pp; English.
XX
CC The invention relates to a short interfering nucleic acid (siNA) molecule
CC that down-regulates expression of a hepatitis B virus (HBV) gene by RNA
CC interference or that inhibits HBV replication. Also disclosed are the
CC following: (i) a method of modulating the expression of a HBV gene in a
CC tissue explant; (ii)) a method of generating a library of siNA constructs
CC having predetermined complexity; (iii) a cell containing one or more siNA
CC molecules; (iv)a kit containing a siNA molecule which can be used to
CC modulate the expression of a HBV target gene in a cell, tissue or
CC organism; and (v) a method for synthesising a siNA molecule. The siNA
CC molecule is adapted for use to treat HBV infection, and comprises a sense
CC and an antisense region, where the antisense region comprises sequence
CC complementary to an RNA sequence encoding HBV and the sense region
CC comprises sequence complementary to the antisense region. The siNA
CC molecule is assembled from 2 nucleic acid fragments, where one fragment
CC comprises the sense region and the second fragment comprises the
CC antisense region of the siNA molecule, where sense region and the
CC antisense region comprise separate oligonucleotides, and are covalently
CC connected via a linker molecule. The linker molecule is a polynucleotide
CC linker or a non-nucleotide linker. The sense region comprises a 3'-
CC terminal overhang and the antisense region comprises a 3'-terminal
CC overhang. The 3'-terminal overhangs each comprise about 2 nucleotides.
CC The antisense region 3'-terminal overhang is complementary to RNA
CC encoding HBV. The siNA is useful for treating human hepatitis B virus
CC infections, and for characterising pathways of gene function, e.g. to
CC inhibit activity of target genes in a pathway to determine the function
CC of uncharacterised genes in gene function analysis. The siNA molecules
CC may also be used in clinical, industrial, environmental, agricultural
CC and/or research settings. The present sequence represents 1 of 1504 HBV
CC siNA molecules of the invention.
XX
SQ Sequence 19 BP; 8 A; 8 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAAGGCA 16
||||||||||||||||
Db 2 AAAGCCACCCAAGGCA 17

RESULT 15
ADM00284
ID ADM00284 standard; RNA; 19 BP.
XX
AC ADM00284;
XX
DT 20-MAY-2004 (first entry)

XX
DE Hepatitis B virus short interfering nucleic acid (siNA) #700.
XX
KW Virucide; Hepatotropic; Gene therapy; ss; short interfering nucleic acid;
KW siNA; hepatitis B virus; HBV; RNA interference.
XX
OS Hepatitis B virus.
XX
PN US2003206887-A1.
XX
PD 06-NOV-2003.
XX
PF 16-SEP-2002; 2002US-00244647.
XX
PR 14-MAY-1992; 92US-00882712.
PR 07-FEB-1994; 94US-00193627.
PR 08-NOV-1999; 99US-00436430.
PR 20-MAR-2000; 2000US-00531025.
PR 09-AUG-2000; 2000US-00636385.
PR 24-OCT-2000; 2000US-00696347.
PR 08-JUN-2001; 2001US-00877478.
PR 08-JUN-2001; 2001US-0296876P.
PR 24-OCT-2001; 2001US-0335059P.
PR 05-DEC-2001; 2001US-0337055P.
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
XX
PA (MORR/) MORRISSEY D.
PA (MCSW/) MCSWIGGEN J A.
PA (BEIG/) BEIGELMAN L.
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PI Morrissey D, Mcswiggen JA, Beigelman L;
XX
DR WPI; 2003-901032/82.
XX
PT New short interfering nucleic acid molecules which down-regulates
PT expression of a hepatitis B virus (HBV) or which inhibits HBV
PT replication, useful for treating human HBV infections or for
PT characterizing gene function.
XX
PS Claim 11; Page 41; 72pp; English.
XX
CC The invention relates to a short interfering nucleic acid (siNA) molecule
CC that down-regulates expression of a hepatitis B virus (HBV) gene by RNA
CC interference or that inhibits HBV replication. Also disclosed are the
CC following: (i) a method of modulating the expression of a HBV gene in a
CC tissue explant; (ii)) a method of generating a library of siNA constructs
CC having predetermined complexity; (iii) a cell containing one or more siNA
CC molecules; (iv)a kit containing a siNA molecule which can be used to
CC modulate the expression of a HBV target gene in a cell, tissue or
CC organism; and (v) a method for synthesising a siNA molecule. The siNA
CC molecule is adapted for use to treat HBV infection, and comprises a sense
CC and an antisense region, where the antisense region comprises sequence
CC complementary to an RNA sequence encoding HBV and the sense region
CC comprises sequence complementary to the antisense region. The siNA
CC molecule is assembled from 2 nucleic acid fragments, where one fragment
CC comprises the sense region and the second fragment comprises the
CC antisense region of the siNA molecule, where sense region and the
CC antisense region comprise separate oligonucleotides, and are covalently
CC connected via a linker molecule. The linker molecule is a polynucleotide
CC linker or a non-nucleotide linker. The sense region comprises a 3'-
CC terminal overhang and the antisense region comprises a 3'-terminal
CC overhang. The 3'-terminal overhangs each comprise about 2 nucleotides.
CC The antisense region 3'-terminal overhang is complementary to RNA
CC encoding HBV. The siNA is useful for treating human hepatitis B virus
CC infections, and for characterising pathways of gene function, e.g. to
CC inhibit activity of target genes in a pathway to determine the function
CC of uncharacterised genes in gene function analysis. The siNA molecules
CC may also be used in clinical, industrial, environmental, agricultural
CC and/or research settings. The present sequence represents 1 of 1504 HBV
CC siNA molecules of the invention.
XX
SQ Sequence 19 BP; 8 A; 7 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AAAGCCACCCAAGGCA 16
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Db          1 AAAGCCACCCAAGGCA 16
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Job time : 265 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 29, 2005, 08:29:34 ; Search time 95 Seconds
(without alignments)
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Perfect score: 16
Sequence: 1 aaagccacccaaggca 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	16	100.0	16	4	US-09-199-269-48	Sequence 48, Appl
	3	16	100.0	16	4	US-09-155-885A-41	Sequence 41, Appl
	4	16	100.0	18	1	US-08-480-220A-22	Sequence 22, Appl
	5	16	100.0	18	2	US-08-864-404-22	Sequence 22, Appl
	6	16	100.0	18	4	US-09-155-885A-49	Sequence 49, Appl
c	7	16	100.0	19	1	US-08-480-220A-21	Sequence 21, Appl
c	8	16	100.0	19	1	US-08-480-220A-25	Sequence 25, Appl
c	9	16	100.0	19	2	US-08-864-404-21	Sequence 21, Appl
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	11	16	100.0	20	2	US-08-501-968-18	Sequence 18, Appl
	12	16	100.0	20	5	PCT-US96-10984-18	Sequence 18, Appl
	13	16	100.0	21	1	US-08-281-106-45	Sequence 45, Appl
	14	16	100.0	21	1	US-08-281-106-47	Sequence 47, Appl
	15	16	100.0	21	1	US-08-287-337A-5	Sequence 5, Appli
	16	16	100.0	21	2	US-08-501-968-7	Sequence 7, Appli
	17	16	100.0	21	4	US-09-199-269-45	Sequence 45, Appl
	18	16	100.0	21	4	US-09-199-269-47	Sequence 47, Appl
	19	16	100.0	21	5	PCT-US95-00508-5	Sequence 5, Appli
	20	16	100.0	21	5	PCT-US96-10984-7	Sequence 7, Appli
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c	23	16	100.0	44	1	US-08-480-220A-19	Sequence 19, Appl
c	24	16	100.0	44	1	US-08-480-220A-20	Sequence 20, Appl
c	25	16	100.0	44	2	US-08-864-404-19	Sequence 19, Appl
c	26	16	100.0	44	2	US-08-864-404-20	Sequence 20, Appl
c	27	16	100.0	50	1	US-08-758-626-25	Sequence 25, Appl
c	28	16	100.0	50	5	PCT-US94-07684-25	Sequence 25, Appl
	29	15	93.8	16	2	US-08-501-968-37	Sequence 37, Appl
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	36	14	87.5	18	2	US-08-501-968-28	Sequence 28, Appl
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	38	14	87.5	20	2	US-08-468-352-13	Sequence 13, Appl
	39	13	81.2	16	1	US-08-281-106-50	Sequence 50, Appl
	40	13	81.2	16	4	US-09-199-269-50	Sequence 50, Appl
	41	13	81.2	20	1	US-08-758-626-14	Sequence 14, Appl
	42	13	81.2	20	5	PCT-US94-07684-14	Sequence 14, Appl
	43	13	81.2	21	1	US-08-281-106-49	Sequence 49, Appl
	44	13	81.2	21	4	US-09-199-269-49	Sequence 49, Appl
	45	13	81.2	25	4	US-09-396-196G-80393	Sequence 80393, A

ALIGNMENTS

RESULT 1
US-08-281-106-48
; Sequence 48, Application US/08281106
; Patent No. 5646262
; GENERAL INFORMATION:
; APPLICANT: KORBA, Brent E.
; APPLICANT: GERIN, John L.
; TITLE OF INVENTION: Antisense Oligonucleotides Against
; TITLE OF INVENTION: Hepatitis B Viral Replication
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,106
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 66683/112/GEUN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 672 5300
; TELEFAX: 202 672 5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: YES
US-08-281-106-48

Query Match 100.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 AAAGCCACCCAAGGCA 16
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RESULT 2
US-09-199-269-48
; Sequence 48, Application US/09199269
; Patent No. 6503533
;   GENERAL INFORMATION:
;        APPLICANT: KORBA, Brent E.
;                   GERIN, John L.
;        TITLE OF INVENTION: Antisense Oligonucleotides Against
;                            Hepatitis B Viral Replication
;        NUMBER OF SEQUENCES: 56
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W.
;             CITY: Washington, D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/199,269
;             FILING DATE: 25-No. 6503533-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/281,106
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BENT, Stephen A.
;             REGISTRATION NUMBER: 29,768
;             REFERENCE/DOCKET NUMBER: 66683/112/GEUN
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202 672 5300
;             TELEFAX: 202 672 5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 48:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        ANTI-SENSE: YES
;        SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-09-199-269-48

  Query Match             100.0%;  Score 16;  DB 4;  Length 16;
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Db          1 AAAGCCACCCAAGGCA 16


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; Sequence 41, Application US/09155885A
; Patent No. 6709812
;   GENERAL INFORMATION:
;        APPLICANT: STUYVER, LIEVEN
;                   ROSSAU, RUDI
;                   MAERTENS, GEERT
;        TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
;        NUMBER OF SEQUENCES: 313
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: NIXON & VANDERHYE P.C.
;             STREET: 1100 NORTH GLEBE ROAD
;             CITY: ARLINGTON
;             STATE: VIRGINIA
;             COUNTRY: U.S.A.
;             ZIP: 22201-4714
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/155,885A
;             FILING DATE: 08-Oct-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/EP97/02002
;             FILING DATE: 21-APR-1997
;             APPLICATION NUMBER: EP 96870053.4
;             FILING DATE: 19-APR-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SADOFF, B.J.
;             REGISTRATION NUMBER: 36,663
;             REFERENCE/DOCKET NUMBER: 2551-5
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (703) 816-4000
;             TELEFAX: (703) 816-4100
;   INFORMATION FOR SEQ ID NO: 41:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-09-155-885A-41

  Query Match             100.0%;  Score 16;  DB 4;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 4
US-08-480-220A-22
; Sequence 22, Application US/08480220A
; Patent No. 5667974
;  GENERAL INFORMATION:
;    APPLICANT:  Birkenmeyer, Larry
;    APPLICANT:  Mushahwar, Isa K.
;    TITLE OF INVENTION:  METHOD FOR DETECTING NUCLEIC ACID
;    TITLE OF INVENTION:  SEQUENCE USING COMPETITIVE AMPLIFICATION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories D377/AP6D
;      STREET:  100 Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC Compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,220A
;      FILING DATE:  07 JUN 1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Porembski, Priscilla E.
;      REGISTRATION NUMBER:  33,207
;      REFERENCE/DOCKET NUMBER:  5770.US.01
;    TELECOMMUNICATION INFORMATION:
```

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;      TELEPHONE:  708/937-6365
;      TELEFAX:  708/938-2623
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  synthetic DNA
;    FEATURE:
;      NAME/KEY:  5' phosphate
;      LOCATION:  1
;    FEATURE:
;      NAME/KEY:  3' fluorescein
;      LOCATION:  18
US-08-480-220A-22

  Query Match             100.0%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 5
US-08-864-404-22
; Sequence 22, Application US/08864404
; Patent No. 5955598
;  GENERAL INFORMATION:
;    APPLICANT:  Birkenmeyer, Larry
;    APPLICANT:  Mushahwar, Isa K.
;    TITLE OF INVENTION:  METHOD FOR DETECTING NUCLEIC ACID
;    TITLE OF INVENTION:  SEQUENCE USING COMPETITIVE AMPLIFICATION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories D377/AP6D
;      STREET:  100 Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60064-35008
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC Compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/864,404
;      FILING DATE:  28-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/480,220
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Porembski, Priscilla E.
;      REGISTRATION NUMBER:  33,207
;      REFERENCE/DOCKET NUMBER:  5770.US.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  708/937-6365
;      TELEFAX:  708/938-2623
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  synthetic DNA
;    FEATURE:
;      NAME/KEY:  5' phosphate
;      LOCATION:  1
;    FEATURE:
;      NAME/KEY:  3' fluorescein
;      LOCATION:  18
US-08-864-404-22

  Query Match             100.0%;  Score 16;  DB 2;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 6
US-09-155-885A-49
; Sequence 49, Application US/09155885A
; Patent No. 6709812
;  GENERAL INFORMATION:
;      APPLICANT: STUYVER, LIEVEN
;                 ROSSAU, RUDI
;                 MAERTENS, GEERT
;      TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
;      NUMBER OF SEQUENCES: 313
;      CORRESPONDENCE ADDRESS:
;           ADDRESSEE: NIXON & VANDERHYE P.C.
;           STREET: 1100 NORTH GLEBE ROAD
;           CITY: ARLINGTON
;           STATE: VIRGINIA
;           COUNTRY: U.S.A.
;           ZIP: 22201-4714
;      COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;      CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/155,885A
;           FILING DATE: 08-Oct-1998
;           CLASSIFICATION: <Unknown>
;      PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: PCT/EP97/02002
;           FILING DATE: 21-APR-1997
;           APPLICATION NUMBER: EP 96870053.4
;           FILING DATE: 19-APR-1996
;      ATTORNEY/AGENT INFORMATION:
;           NAME: SADOFF, B.J.
;           REGISTRATION NUMBER: 36,663
;           REFERENCE/DOCKET NUMBER: 2551-5
;      TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (703) 816-4000
;           TELEFAX: (703) 816-4100
;  INFORMATION FOR SEQ ID NO: 49:
;      SEQUENCE CHARACTERISTICS:
;           LENGTH: 18 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;      MOLECULE TYPE: DNA (genomic)
;      HYPOTHETICAL: NO
;      ANTI-SENSE: NO
;      SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-09-155-885A-49

  Query Match             100.0%;  Score 16;  DB 4;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16
```

```
RESULT 7
US-08-480-220A-21/c
; Sequence 21, Application US/08480220A
; Patent No. 5667974
;  GENERAL INFORMATION:
;    APPLICANT:  Birkenmeyer, Larry
;    APPLICANT:  Mushahwar, Isa K.
;    TITLE OF INVENTION:  METHOD FOR DETECTING NUCLEIC ACID
;    TITLE OF INVENTION:  SEQUENCE USING COMPETITIVE AMPLIFICATION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories D377/AP6D
;      STREET:  100 Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC Compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,220A
;      FILING DATE:  07 JUN 1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Porembski, Priscilla E.
;      REGISTRATION NUMBER:  33,207
;      REFERENCE/DOCKET NUMBER:  5770.US.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  708/937-6365
;      TELEFAX:  708/938-2623
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  synthetic DNA
;    FEATURE:
;      NAME/KEY:  5' fluorescein
;      LOCATION:  1
US-08-480-220A-21

  Query Match             100.0%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         18 AAAGCCACCCAAGGCA 3


RESULT 8
US-08-480-220A-25/c
; Sequence 25, Application US/08480220A
; Patent No. 5667974
;  GENERAL INFORMATION:
;    APPLICANT:  Birkenmeyer, Larry
;    APPLICANT:  Mushahwar, Isa K.
;    TITLE OF INVENTION:  METHOD FOR DETECTING NUCLEIC ACID
;    TITLE OF INVENTION:  SEQUENCE USING COMPETITIVE AMPLIFICATION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories D377/AP6D
;      STREET:  100 Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC Compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,220A
;      FILING DATE:  07 JUN 1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Porembski, Priscilla E.
;      REGISTRATION NUMBER:  33,207
;      REFERENCE/DOCKET NUMBER:  5770.US.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  708/937-6365
;      TELEFAX:  708/938-2623
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  synthetic DNA
;    FEATURE:
;      NAME/KEY:  5' fluorescein
;      LOCATION:  1
US-08-480-220A-25

  Query Match             100.0%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         18 AAAGCCACCCAAGGCA 3


RESULT 9
US-08-864-404-21/c
; Sequence 21, Application US/08864404
; Patent No. 5955598
;  GENERAL INFORMATION:
;    APPLICANT:  Birkenmeyer, Larry
;    APPLICANT:  Mushahwar, Isa K.
;    TITLE OF INVENTION:  METHOD FOR DETECTING NUCLEIC ACID
;    TITLE OF INVENTION:  SEQUENCE USING COMPETITIVE AMPLIFICATION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories D377/AP6D
;      STREET:  100 Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60064-35008
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC Compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/864,404
;      FILING DATE:  28-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/480,220
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Porembski, Priscilla E.
;      REGISTRATION NUMBER:  33,207
;      REFERENCE/DOCKET NUMBER:  5770.US.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  708/937-6365
```

```
;      TELEFAX:  708/938-2623
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  synthetic DNA
;    FEATURE:
;      NAME/KEY:  5' fluorescein
;      LOCATION:  1
US-08-864-404-21

  Query Match            100.0%;  Score 16;  DB 2;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 23;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         18 AAAGCCACCCAAGGCA 3


RESULT 10
US-08-864-404-25/c
; Sequence 25, Application US/08864404
; Patent No. 5955598
;  GENERAL INFORMATION:
;    APPLICANT:  Birkenmeyer, Larry
;    APPLICANT:  Mushahwar, Isa K.
;    TITLE OF INVENTION:  METHOD FOR DETECTING NUCLEIC ACID
;    TITLE OF INVENTION:  SEQUENCE USING COMPETITIVE AMPLIFICATION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories D377/AP6D
;      STREET:  100 Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60064-35008
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC Compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/864,404
;      FILING DATE:  28-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/480,220
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Porembski, Priscilla E.
;      REGISTRATION NUMBER:  33,207
;      REFERENCE/DOCKET NUMBER:  5770.US.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  708/937-6365
;      TELEFAX:  708/938-2623
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  synthetic DNA
;    FEATURE:
;      NAME/KEY:  5' fluorescein
;      LOCATION:  1
US-08-864-404-25

  Query Match            100.0%;  Score 16;  DB 2;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 23;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         18 AAAGCCACCCAAGGCA 3


RESULT 11
US-08-501-968-18
; Sequence 18, Application US/08501968
; Patent No. 5985662
;  GENERAL INFORMATION:
;    APPLICANT:  Kevin Anderson and Lex Cowsert
;    TITLE OF INVENTION:  Antisense Inhibition of Hepatitis B
;    TITLE OF INVENTION:  Virus Replication
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jane Massey Licata, Esq.
;      STREET:  210 Lake Drive East, Suite 201
;      CITY:  Cherry Hill
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08002
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;      COMPUTER:  IBM 486
;      OPERATING SYSTEM:  WINDOWS FOR WORKGROUPS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/501,968
;      FILING DATE:  herewith
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:  none
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jane Massey Licata
;      REGISTRATION NUMBER:  32,257
;      REFERENCE/DOCKET NUMBER:  ISPH-0128
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (609) 779-2400
;      TELEFAX:  (609) 779-8488
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  YES
US-08-501-968-18

  Query Match            100.0%;  Score 16;  DB 2;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 23;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 12
PCT-US96-10984-18
; Sequence 18, Application PC/TUS9610984
;  GENERAL INFORMATION:
;    APPLICANT:  Kevin Anderson and Lex Cowsert
;    TITLE OF INVENTION:  Antisense Inhibition of Hepatitis B
;    TITLE OF INVENTION:  Virus Replication
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jane Massey Licata, Esq.
;      STREET:  210 Lake Drive East, Suite 201
;      CITY:  Cherry Hill
;      STATE:  NJ
```

```
;       COUNTRY:  USA
;       ZIP:  08002
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 Mb
;       MEDIUM TYPE:  STORAGE
;       COMPUTER:  IBM 486
;       OPERATING SYSTEM:  WINDOWS FOR WORKGROUPS
;       SOFTWARE:  WORDPERFECT 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US96/10984
;       FILING DATE:  herewith
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:  none
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Jane Massey Licata
;       REGISTRATION NUMBER:  32,257
;       REFERENCE/DOCKET NUMBER:  ISPH-0128
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (609) 779-2400
;       TELEFAX:  (609) 779-8488
;   INFORMATION FOR SEQ ID NO:  18:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  20 nucleotides
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  YES
PCT-US96-10984-18

  Query Match             100.0%;  Score 16;  DB 5;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 13
US-08-281-106-45
; Sequence 45, Application US/08281106
; Patent No. 5646262
;  GENERAL INFORMATION:
;    APPLICANT:  KORBA, Brent E.
;    APPLICANT:  GERIN, John L.
;    TITLE OF INVENTION:  Antisense Oligonucleotides Against
;    TITLE OF INVENTION:  Hepatitis B Viral Replication
;    NUMBER OF SEQUENCES:  56
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W.
;      CITY:  Washington, D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/281,106
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  66683/112/GEUN
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202 672 5300
;      TELEFAX:  202 672 5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  45:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    ANTI-SENSE:  YES
US-08-281-106-45

  Query Match             100.0%;  Score 16;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 14
US-08-281-106-47
; Sequence 47, Application US/08281106
; Patent No. 5646262
;  GENERAL INFORMATION:
;    APPLICANT:  KORBA, Brent E.
;    APPLICANT:  GERIN, John L.
;    TITLE OF INVENTION:  Antisense Oligonucleotides Against
;    TITLE OF INVENTION:  Hepatitis B Viral Replication
;    NUMBER OF SEQUENCES:  56
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W.
;      CITY:  Washington, D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/281,106
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  66683/112/GEUN
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202 672 5300
;      TELEFAX:  202 672 5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  47:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    ANTI-SENSE:  YES
US-08-281-106-47

  Query Match             100.0%;  Score 16;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 23;
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Qy          1 AAAGCCACCCAAGGCA 16
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Db          6 AAAGCCACCCAAGGCA 21


RESULT 15
US-08-287-337A-5
; Sequence 5, Application US/08287337A
; Patent No. 5728518
;  GENERAL INFORMATION:
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;    APPLICANT:  Ellen Carmichael
;    TITLE OF INVENTION:  ANTIVIRAL OLIGONUCLOETIDE
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street, Suite 510
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/287,337A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Giulio A. DeConti, Jr.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  TTI-109
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-287-337A-5

  Query Match           100.0%;  Score 16;  DB 1;  Length 21;
  Best Local Similarity  100.0%;  Pred. No. 23;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
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Db          6 AAAGCCACCCAAGGCA 21


Search completed: March 29, 2005, 09:35:41
Job time : 95 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 29, 2005, 09:03:35 ; Search time 305 Seconds
(without alignments)
312.621 Million cell updates/sec

Title: US-09-888-164-29
Perfect score: 16
Sequence: 1 aaagccacccaaggca 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5552208 seqs, 2979665951 residues

Total number of hits satisfying chosen parameters: 5243446

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	16	100.0	16	10	US-09-888-164-29	Sequence 29, Appl
	2	16	100.0	16	17	US-10-453-792-41	Sequence 41, Appl
c	3	16	100.0	17	10	US-09-877-478-1755	Sequence 1755, Ap
c	4	16	100.0	17	10	US-09-877-478-2378	Sequence 2378, Ap
c	5	16	100.0	17	17	US-10-342-902-1755	Sequence 1755, Ap
c	6	16	100.0	17	17	US-10-342-902-2378	Sequence 2378, Ap
c	7	16	100.0	17	18	US-10-669-841-1755	Sequence 1755, Ap
c	8	16	100.0	17	18	US-10-669-841-2181	Sequence 2181, Ap
	9	16	100.0	18	17	US-10-453-792-49	Sequence 49, Appl
c	10	16	100.0	19	17	US-10-244-647-54	Sequence 54, Appl
c	11	16	100.0	19	17	US-10-244-647-574	Sequence 574, App
c	12	16	100.0	19	17	US-10-244-647-576	Sequence 576, App
c	13	16	100.0	19	17	US-10-244-647-577	Sequence 577, App
	14	16	100.0	19	17	US-10-244-647-700	Sequence 700, App
	15	16	100.0	19	17	US-10-244-647-1220	Sequence 1220, Ap
	16	16	100.0	19	17	US-10-244-647-1222	Sequence 1222, Ap
	17	16	100.0	19	17	US-10-244-647-1223	Sequence 1223, Ap
c	18	16	100.0	23	17	US-10-244-647-1296	Sequence 1296, Ap
c	19	15	93.8	17	10	US-09-877-478-2377	Sequence 2377, Ap
c	20	15	93.8	17	17	US-10-342-902-2377	Sequence 2377, Ap
c	21	15	93.8	17	18	US-10-669-841-2180	Sequence 2180, Ap
c	22	15	93.8	19	17	US-10-244-647-64	Sequence 64, Appl
	23	15	93.8	19	17	US-10-244-647-710	Sequence 710, App
c	24	15	93.8	30	18	US-10-343-324-8	Sequence 8, Appli
c	25	15	93.8	33	17	US-10-147-679A-21	Sequence 21, Appl
	26	14.4	90.0	20	16	US-10-032-585-5187	Sequence 5187, Ap
c	27	14.4	90.0	25	19	US-10-809-189-99805	Sequence 99805, A
c	28	14.4	90.0	41	17	US-10-035-833A-2279	Sequence 2279, Ap
c	29	14.4	90.0	41	17	US-10-035-833A-3685	Sequence 3685, Ap
c	30	14	87.5	17	10	US-09-877-478-418	Sequence 418, App
c	31	14	87.5	17	10	US-09-877-478-2379	Sequence 2379, Ap
c	32	14	87.5	17	17	US-10-342-902-418	Sequence 418, App
c	33	14	87.5	17	17	US-10-342-902-2379	Sequence 2379, Ap
c	34	14	87.5	17	18	US-10-669-841-418	Sequence 418, App
c	35	14	87.5	17	18	US-10-669-841-2182	Sequence 2182, Ap
c	36	14	87.5	19	17	US-10-244-647-61	Sequence 61, Appl
	37	14	87.5	19	17	US-10-244-647-707	Sequence 707, App
c	38	14	87.5	21	17	US-10-244-647-1340	Sequence 1340, Ap
	39	14	87.5	21	17	US-10-244-647-1344	Sequence 1344, Ap
c	40	14	87.5	21	18	US-10-444-853A-179	Sequence 179, App
	41	14	87.5	21	18	US-10-444-853A-183	Sequence 183, App
c	42	14	87.5	21	19	US-10-757-803-179	Sequence 179, App
	43	14	87.5	21	19	US-10-757-803-183	Sequence 183, App
c	44	14	87.5	21	19	US-10-826-966-179	Sequence 179, App
	45	14	87.5	21	19	US-10-826-966-183	Sequence 183, App

ALIGNMENTS

RESULT 1
US-09-888-164-29
; Sequence 29, Application US/09888164
; Publication No. US20030119724A1
; GENERAL INFORMATION:
; APPLICANT: Ts'o, Paul O.P.
; APPLICANT: Hangeland, Jon
; APPLICANT: Deamond, Scott
; APPLICANT: Roby, Clinton
; TITLE OF INVENTION: LIGANDS TO ENHANCE CELLULAR UPTAKE OF BIOMOLECULES
; FILE REFERENCE: 212241
; CURRENT APPLICATION NUMBER: US/09/888,164
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 09/282,455
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 08/755,062
; PRIOR FILING DATE: 1996-11-22
; PRIOR APPLICATION NUMBER: 60/007,480
; PRIOR FILING DATE: 1995-11-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Control oligomer
US-09-888-164-29

Query Match 100.0%; Score 16; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAAGGCA 16

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Db          1 AAAGCCACCCAAGGCA 16


RESULT 2
US-10-453-792-41
; Sequence 41, Application US/10453792
; Publication No. US20040029110A1
;   GENERAL INFORMATION:
;        APPLICANT: STUYVER, LIEVEN
;                   ROSSAU, RUDI
;                   MAERTENS, GEERT
;        TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
;        NUMBER OF SEQUENCES: 313
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: NIXON & VANDERHYE P.C.
;             STREET: 1100 NORTH GLEBE ROAD
;             CITY: ARLINGTON
;             STATE: VIRGINIA
;             COUNTRY: U.S.A.
;             ZIP: 22201-4714
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/453,792
;             FILING DATE: 04-Jun-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/155,885A
;             FILING DATE: 08-Oct-1998
;             APPLICATION NUMBER: PCT/EP97/02002
;             FILING DATE: 21-APR-1997
;             APPLICATION NUMBER: EP 96870053.4
;             FILING DATE: 19-APR-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SADOFF, B.J.
;             REGISTRATION NUMBER: 36,663
;             REFERENCE/DOCKET NUMBER: 2551-5
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (703) 816-4000
;             TELEFAX: (703) 816-4100
;   INFORMATION FOR SEQ ID NO: 41:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-453-792-41

  Query Match             100.0%;  Score 16;  DB 17;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
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Db          1 AAAGCCACCCAAGGCA 16


RESULT 3
US-09-877-478-1755/c
; Sequence 1755, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Draper, Kenneth
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Morrissey, Dave
;  TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
;  FILE REFERENCE: MBHB00-845-H (400/029)
;  CURRENT APPLICATION NUMBER: US/09/877,478
;  CURRENT FILING DATE:  2001-12-31
;  PRIOR APPLICATION NUMBER: US 07/882,712
;  PRIOR FILING DATE: 1992-05-14
;  PRIOR APPLICATION NUMBER: US 09/531,025
;  PRIOR FILING DATE: 2000-03-20
;  PRIOR APPLICATION NUMBER: US 09/636,385
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: US 09/696,347
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 08/193,627
;  PRIOR FILING DATE: 1994-02-07
;  PRIOR APPLICATION NUMBER: US 08/433,993
;  PRIOR FILING DATE: 1995-05-04
;  PRIOR APPLICATION NUMBER: US 08/434,504
;  PRIOR FILING DATE: 1995-05-04
;  PRIOR APPLICATION NUMBER: US 09/436,430
;  PRIOR FILING DATE: 1999-11-08
;  NUMBER OF SEQ ID NOS: 6586
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1755
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Hepatitis B virus
US-09-877-478-1755

  Query Match             100.0%;  Score 16;  DB 10;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         16 AAAGCCACCCAAGGCA 1


RESULT 4
US-09-877-478-2378/c
; Sequence 2378, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Draper, Kenneth
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Morrissey, Dave
;  TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
;  FILE REFERENCE: MBHB00-845-H (400/029)
;  CURRENT APPLICATION NUMBER: US/09/877,478
;  CURRENT FILING DATE:  2001-12-31
;  PRIOR APPLICATION NUMBER: US 07/882,712
;  PRIOR FILING DATE: 1992-05-14
;  PRIOR APPLICATION NUMBER: US 09/531,025
;  PRIOR FILING DATE: 2000-03-20
;  PRIOR APPLICATION NUMBER: US 09/636,385
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: US 09/696,347
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 08/193,627
;  PRIOR FILING DATE: 1994-02-07
;  PRIOR APPLICATION NUMBER: US 08/433,993
;  PRIOR FILING DATE: 1995-05-04
;  PRIOR APPLICATION NUMBER: US 08/434,504
;  PRIOR FILING DATE: 1995-05-04
;  PRIOR APPLICATION NUMBER: US 09/436,430
;  PRIOR FILING DATE: 1999-11-08
;  NUMBER OF SEQ ID NOS: 6586
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2378
;   LENGTH: 17
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;   TYPE: RNA
;   ORGANISM: Hepatitis B virus
US-09-877-478-2378

  Query Match             100.0%;  Score 16;  DB 10;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
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Db         17 AAAGCCACCCAAGGCA 2


RESULT 5
US-10-342-902-1755/c
; Sequence 1755, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  Draper, Kenneth
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Morrissey, Dave
;  TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
;  FILE REFERENCE: 400/075 (MBHB00-845-I)
;  CURRENT APPLICATION NUMBER: US/10/342,902
;  CURRENT FILING DATE:  2003-01-15
;  PRIOR APPLICATION NUMBER: US 09/877,478
;  PRIOR FILING DATE: 2001-06-08
;  PRIOR APPLICATION NUMBER: US 09/531,025
;  PRIOR FILING DATE: 2000-03-20
;  PRIOR APPLICATION NUMBER: US 09/636,385
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: US 09/696,347
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 08/193,627
;  PRIOR FILING DATE: 1994-02-07
;  PRIOR APPLICATION NUMBER: US 07/882,712
;  PRIOR FILING DATE: 1992-05-14
;  PRIOR APPLICATION NUMBER: US 09/436,430
;  PRIOR FILING DATE: 1999-11-08
;  NUMBER OF SEQ ID NOS: 6592
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1755
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Hepatitis B virus
US-10-342-902-1755

  Query Match             100.0%;  Score 16;  DB 17;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         16 AAAGCCACCCAAGGCA 1


RESULT 6
US-10-342-902-2378/c
; Sequence 2378, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  Draper, Kenneth
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Morrissey, Dave
;  TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
;  FILE REFERENCE: 400/075 (MBHB00-845-I)
;  CURRENT APPLICATION NUMBER: US/10/342,902
;  CURRENT FILING DATE:  2003-01-15
;  PRIOR APPLICATION NUMBER: US 09/877,478
;  PRIOR FILING DATE: 2001-06-08
;  PRIOR APPLICATION NUMBER: US 09/531,025
;  PRIOR FILING DATE: 2000-03-20
;  PRIOR APPLICATION NUMBER: US 09/636,385
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: US 09/696,347
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 08/193,627
;  PRIOR FILING DATE: 1994-02-07
;  PRIOR APPLICATION NUMBER: US 07/882,712
;  PRIOR FILING DATE: 1992-05-14
;  PRIOR APPLICATION NUMBER: US 09/436,430
;  PRIOR FILING DATE: 1999-11-08
;  NUMBER OF SEQ ID NOS: 6592
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2378
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Hepatitis B virus
US-10-342-902-2378

  Query Match             100.0%;  Score 16;  DB 17;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         17 AAAGCCACCCAAGGCA 2


RESULT 7
US-10-669-841-1755/c
; Sequence 1755, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  Lawrence, Blatt
;  APPLICANT:  Dennis, Macejak
;  APPLICANT:  James, McSwiggen
;  APPLICANT:  David, Morrissey
;  APPLICANT:  Pamela, Pavco
;  APPLICANT:  Patrice, Lee
;  APPLICANT:  Kenneth, Draper
;  APPLICANT:  Elisabeth, Roberts
;  TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA
;  TITLE OF INVENTION:  VIRUS REPLICATION
;  FILE REFERENCE: 400/042US  (MBHB02-249-E)
;  CURRENT APPLICATION NUMBER: US/10/669,841
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: PCT/US02/09187
;  PRIOR FILING DATE: 2002-03-26
;  PRIOR APPLICATION NUMBER: US 60/296,876
;  PRIOR FILING DATE: 2001-06-08
;  PRIOR APPLICATION NUMBER: US 60/335,059
;  PRIOR FILING DATE: 2001-10-24
;  PRIOR APPLICATION NUMBER: US 60/337,055
;  PRIOR FILING DATE: 2001-12-05
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/363,124
;  PRIOR FILING DATE: 2002-03-11
;  PRIOR APPLICATION NUMBER: US 09/817,879
;  PRIOR FILING DATE: 2001-03-26
;  PRIOR APPLICATION NUMBER: US 09/740,332
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: US 09/611,931
;  PRIOR FILING DATE: 2000-07-07
;  PRIOR APPLICATION NUMBER: US 09/504,321
;  PRIOR FILING DATE: 2000-02-15
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 16207
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1755
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;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Hepatitis B Virus
US-10-669-841-1755

  Query Match             100.0%;  Score 16;  DB 18;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         16 AAAGCCACCCAAGGCA 1


RESULT 8
US-10-669-841-2181/c
; Sequence 2181, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  Lawrence, Blatt
;  APPLICANT:  Dennis, Macejak
;  APPLICANT:  James, McSwiggen
;  APPLICANT:  David, Morrissey
;  APPLICANT:  Pamela, Pavco
;  APPLICANT:  Patrice, Lee
;  APPLICANT:  Kenneth, Draper
;  APPLICANT:  Elisabeth, Roberts
;  TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA
;  TITLE OF INVENTION:  VIRUS REPLICATION
;  FILE REFERENCE: 400/042US  (MBHB02-249-E)
;  CURRENT APPLICATION NUMBER: US/10/669,841
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: PCT/US02/09187
;  PRIOR FILING DATE: 2002-03-26
;  PRIOR APPLICATION NUMBER: US 60/296,876
;  PRIOR FILING DATE: 2001-06-08
;  PRIOR APPLICATION NUMBER: US 60/335,059
;  PRIOR FILING DATE: 2001-10-24
;  PRIOR APPLICATION NUMBER: US 60/337,055
;  PRIOR FILING DATE: 2001-12-05
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/363,124
;  PRIOR FILING DATE: 2002-03-11
;  PRIOR APPLICATION NUMBER: US 09/817,879
;  PRIOR FILING DATE: 2001-03-26
;  PRIOR APPLICATION NUMBER: US 09/740,332
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: US 09/611,931
;  PRIOR FILING DATE: 2000-07-07
;  PRIOR APPLICATION NUMBER: US 09/504,321
;  PRIOR FILING DATE: 2000-02-15
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 16207
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2181
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Hepatitis B Virus
US-10-669-841-2181

  Query Match             100.0%;  Score 16;  DB 18;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         17 AAAGCCACCCAAGGCA 2


RESULT 9
US-10-453-792-49
; Sequence 49, Application US/10453792
; Publication No. US20040029110A1
;   GENERAL INFORMATION:
;        APPLICANT: STUYVER, LIEVEN
;                   ROSSAU, RUDI
;                   MAERTENS, GEERT
;        TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
;        NUMBER OF SEQUENCES: 313
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: NIXON & VANDERHYE P.C.
;             STREET: 1100 NORTH GLEBE ROAD
;             CITY: ARLINGTON
;             STATE: VIRGINIA
;             COUNTRY: U.S.A.
;             ZIP: 22201-4714
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/453,792
;             FILING DATE: 04-Jun-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/155,885A
;             FILING DATE: 08-Oct-1998
;             APPLICATION NUMBER: PCT/EP97/02002
;             FILING DATE: 21-APR-1997
;             APPLICATION NUMBER: EP 96870053.4
;             FILING DATE: 19-APR-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SADOFF, B.J.
;             REGISTRATION NUMBER: 36,663
;             REFERENCE/DOCKET NUMBER: 2551-5
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (703) 816-4000
;             TELEFAX: (703) 816-4100
;   INFORMATION FOR SEQ ID NO: 49:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-453-792-49

  Query Match             100.0%;  Score 16;  DB 17;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 10
US-10-244-647-54/c
; Sequence 54, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceutical, Inc.
;  APPLICANT:  Morrissey, David
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV) U
;  TITLE OF INVENTION:  Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/060 (MBHB02-1000)
;  CURRENT APPLICATION NUMBER: US/10/244,647
;  CURRENT FILING DATE:  2003-04-14
```

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;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/393,924
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: PCT US02/09187
;  PRIOR FILING DATE: 2002-03-26
;  PRIOR APPLICATION NUMBER: US 60/296,876
;  PRIOR FILING DATE: 2001-06-08
;  NUMBER OF SEQ ID NOS: 1524
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 54
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target sequence/siNA sense r
US-10-244-647-54

  Query Match           100.0%;  Score 16;  DB 17;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         19 AAAGCCACCCAAGGCA 4


RESULT 11
US-10-244-647-574/c
; Sequence 574, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceutical, Inc.
;  APPLICANT:  Morrissey, David
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV) U
;  TITLE OF INVENTION:  Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/060 (MBHB02-1000)
;  CURRENT APPLICATION NUMBER: US/10/244,647
;  CURRENT FILING DATE:  2003-04-14
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/393,924
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: PCT US02/09187
;  PRIOR FILING DATE: 2002-03-26
;  PRIOR APPLICATION NUMBER: US 60/296,876
;  PRIOR FILING DATE: 2001-06-08
;  NUMBER OF SEQ ID NOS: 1524
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 574
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target sequence/siNA sense r
US-10-244-647-574

  Query Match           100.0%;  Score 16;  DB 17;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         17 AAAGCCACCCAAGGCA 2


RESULT 12
US-10-244-647-576/c
; Sequence 576, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceutical, Inc.
;  APPLICANT:  Morrissey, David
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV) U
;  TITLE OF INVENTION:  Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/060 (MBHB02-1000)
;  CURRENT APPLICATION NUMBER: US/10/244,647
;  CURRENT FILING DATE:  2003-04-14
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/393,924
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: PCT US02/09187
;  PRIOR FILING DATE: 2002-03-26
;  PRIOR APPLICATION NUMBER: US 60/296,876
;  PRIOR FILING DATE: 2001-06-08
;  NUMBER OF SEQ ID NOS: 1524
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 576
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target sequence/siNA sense r
US-10-244-647-576

  Query Match           100.0%;  Score 16;  DB 17;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db         16 AAAGCCACCCAAGGCA 1


RESULT 13
US-10-244-647-577/c
; Sequence 577, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceutical, Inc.
;  APPLICANT:  Morrissey, David
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV) U
;  TITLE OF INVENTION:  Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/060 (MBHB02-1000)
;  CURRENT APPLICATION NUMBER: US/10/244,647
;  CURRENT FILING DATE:  2003-04-14
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/393,924
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: PCT US02/09187
;  PRIOR FILING DATE: 2002-03-26
;  PRIOR APPLICATION NUMBER: US 60/296,876
;  PRIOR FILING DATE: 2001-06-08
;  NUMBER OF SEQ ID NOS: 1524
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 577
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target sequence/siNA sense r
US-10-244-647-577

  Query Match           100.0%;  Score 16;  DB 17;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
```

```
              ||||||||||||||||
Db         18 AAAGCCACCCAAGGCA 3


RESULT 14
US-10-244-647-700
; Sequence 700, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceutical, Inc.
;  APPLICANT:  Morrissey, David
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV) U
;  TITLE OF INVENTION:  Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/060 (MBHB02-1000)
;  CURRENT APPLICATION NUMBER: US/10/244,647
;  CURRENT FILING DATE:  2003-04-14
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/393,924
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: PCT US02/09187
;  PRIOR FILING DATE: 2002-03-26
;  PRIOR APPLICATION NUMBER: US 60/296,876
;  PRIOR FILING DATE: 2001-06-08
;  NUMBER OF SEQ ID NOS: 1524
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 700
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-244-647-700

  Query Match             100.0%;  Score 16;  DB 17;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          1 AAAGCCACCCAAGGCA 16


RESULT 15
US-10-244-647-1220
; Sequence 1220, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceutical, Inc.
;  APPLICANT:  Morrissey, David
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV) U
;  TITLE OF INVENTION:  Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/060 (MBHB02-1000)
;  CURRENT APPLICATION NUMBER: US/10/244,647
;  CURRENT FILING DATE:  2003-04-14
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/393,924
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: PCT US02/09187
;  PRIOR FILING DATE: 2002-03-26
;  PRIOR APPLICATION NUMBER: US 60/296,876
;  PRIOR FILING DATE: 2001-06-08
;  NUMBER OF SEQ ID NOS: 1524
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1220
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-244-647-1220

  Query Match             100.0%;  Score 16;  DB 17;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||||||||||
Db          3 AAAGCCACCCAAGGCA 18


Search completed: March 29, 2005, 10:26:46
Job time : 306 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 29, 2005, 08:23:24 ; Search time 1827 Seconds
(without alignments)
333.349 Million cell updates/sec

Title: US-09-888-164-29
Perfect score: 16
Sequence: 1 aaagccacccaaggca 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	12.8	80.0	34	9	AJ597693	Arabidops
	2	12.8	80.0	40	8	BZ288461	BZ288461 SALK_0218
	3	12.8	80.0	45	9	BX227597	BX227597 Danio rer
c	4	12.4	77.5	48	9	BX223641	BX223641 Danio rer
	5	11.8	73.8	46	9	CC798987	CC798987 RRK477 Ba
	6	11.8	73.8	50	1	AU104174	AU104174 AU104174
	7	11.2	70.0	20	7	CO794661	NT144B_A0
	8	11.2	70.0	35	5	BX567608	BX567608 BX567608
c	9	11.2	70.0	36	8	AZ505596	AZ505596 1M0346B24
	10	11.2	70.0	37	1	AI597737	AI597737 tu91b01.x
	11	11.2	70.0	37	2	BF211603	BF211603 601812103
	12	11.2	70.0	40	1	AI690571	AI690571 tq02a02.x
c	13	11.2	70.0	43	7	R50470	R50470 yj56h09.r1
	14	11.2	70.0	46	1	AI355812	AI355812 qt94h07.x
	15	11.2	70.0	46	7	R78378	R78378 yi78d11.s1
c	16	11.2	70.0	48	8	CC199771	CC199771 XH136 Bay
	17	11.2	70.0	48	9	AL759212	AL759212 Arabidops
c	18	11.2	70.0	49	9	AL770576	AL770576 Arabidops
	19	11.2	70.0	49	9	CL656736	PRI0127b_
	20	11.2	70.0	50	1	AU102275	AU102275 AU102275
	21	11.2	70.0	50	1	AU102279	AU102279 AU102279
	22	11.2	70.0	50	1	AU102280	AU102280 AU102280
c	23	11.2	70.0	50	1	AU107174	AU107174 AU107174
c	24	11.2	70.0	50	9	CR181440	CR181440 Forward s
	25	11.2	70.0	50	9	CG724386	CG724386 1119081A0
c	26	11	68.8	36	1	AJ730200	AJ730200 AJ730200
c	27	11	68.8	37	1	AA906759	AA906759 ok78e10.s
c	28	10.8	67.5	23	8	AZ957578	AZ957578 2M0224D05
	29	10.8	67.5	26	9	CG722656	CG722656 1119072H1
	30	10.8	67.5	27	8	AZ484720	AZ484720 1M0311H21
	31	10.8	67.5	29	9	CG724617	CG724617 1119082A0
c	32	10.8	67.5	33	2	BF026752	BF026752 601671969
c	33	10.8	67.5	33	8	AZ789688	AZ789688 2M0037O08
c	34	10.8	67.5	34	8	AZ427682	AZ427682 1M0209I15
	35	10.8	67.5	37	1	AI683766	AI683766 tw53g05.x
c	36	10.8	67.5	37	8	AZ648227	AZ648227 1M0517G12
c	37	10.8	67.5	38	9	CG426349	CG426349 01S0583-0
	38	10.8	67.5	40	1	AI609582	AI609582 tw28c02.x
c	39	10.8	67.5	41	8	AZ807826	AZ807826 2M0070L19
c	40	10.8	67.5	42	4	BJ037294	BJ037294 BJ037294
	41	10.8	67.5	43	9	BX190610	BX190610 Danio rer
c	42	10.8	67.5	45	8	AZ767497	AZ767497 1M0566O08
c	43	10.8	67.5	45	8	CC022480	CC022480 3591_1_2_
c	44	10.8	67.5	45	9	BX660740	BX660740 Arabidops
c	45	10.8	67.5	50	1	AU102426	AU102426 AU102426

ALIGNMENTS

RESULT 1
AJ597693/c
LOCUS AJ597693 34 bp DNA linear GSS 15-JAN-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 455C03, genomic survey sequence.
ACCESSION AJ597693
VERSION AJ597693.1 GI:37947321
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446565
REFERENCE 2 (bases 1 to 34)
AUTHORS Balzergue,S.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
FEATURES Location/Qualifiers
source 1. .34
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="455C03"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
misc_feature 1. .34

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                     /note="T-DNA flanking sequence
                     left border"
ORIGIN

  Query Match             80.0%;  Score 12.8;  DB 9;  Length 34;
  Best Local Similarity   87.5%;  Pred. No. 6.4e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              | ||||||||| ||||
Db         22 ACAGCCACCCATGGCA 7


RESULT 2
BZ288461
LOCUS       BZ288461                 40 bp    DNA     linear   GSS 24-OCT-2002
DEFINITION  SALK_021847.34.20.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_021847.34.20.x, genomic
            survey sequence.
ACCESSION   BZ288461
VERSION     BZ288461.1  GI:24328219
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /ecotype="Col-0"
                     /db_xref="taxon:3702"
                     /clone="SALK_021847.34.20.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
ORIGIN

  Query Match             80.0%;  Score 12.8;  DB 8;  Length 40;
  Best Local Similarity   87.5%;  Pred. No. 6.4e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||||||  ||||||
Db         20 AAAGCCACTGAAGGCA 35


RESULT 3
BX227597
LOCUS       BX227597                 45 bp    DNA     linear   GSS 29-JAN-2003
DEFINITION  Danio rerio genomic clone DKEY-281G18, genomic survey sequence.
ACCESSION   BX227597
VERSION     BX227597.1  GI:28061747
KEYWORDS    GSS.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   Humphray,S.J., Huckle,E. and Durham,J.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the T7 end of BAC 281G18. 281G18
            is part of the Daniokey BAC Library created by R. Plasterk and N.V.
            Keygene. Further details:
            http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="Danio rerio"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7955"
                     /clone="DKEY-281G18"
                     /tissue_type="Testis"
                     /note="vector pIndigoBAC-536"
ORIGIN

  Query Match             80.0%;  Score 12.8;  DB 9;  Length 45;
  Best Local Similarity   87.5%;  Pred. No. 6.5e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||| ||||||||  |||
Db          1 AAACCCACCCAAAGCA 16


RESULT 4
BX223641/c
LOCUS       BX223641                 48 bp    DNA     linear   GSS 29-JAN-2003
DEFINITION  Danio rerio genomic clone DKEY-268K13, genomic survey sequence.
ACCESSION   BX223641
VERSION     BX223641.1  GI:28055527
KEYWORDS    GSS.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Humphray,S.J., Huckle,E. and Durham,J.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the SP6 end of BAC 268K13. 268K13
            is part of the Daniokey BAC Library created by R. Plasterk and N.V.
            Keygene. Further details:
            http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES             Location/Qualifiers
     source          1. .48
                     /organism="Danio rerio"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7955"
                     /clone="DKEY-268K13"
                     /tissue_type="Testis"
                     /note="vector pIndigoBAC-536"
ORIGIN

  Query Match             77.5%;  Score 12.4;  DB 9;  Length 48;
  Best Local Similarity   92.9%;  Pred. No. 1.1e+05;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          3 AGCCACCCAAGGCA 16
              ||||||||||| ||
Db         20 AGCCACCCAAGTCA 7


RESULT 5
CC798987
LOCUS       CC798987                 46 bp    mRNA    linear   GSS 01-APR-2004
DEFINITION  RRK477 BayGenomics Gene Trap Library pGT2Lxf Mus musculus cDNA,
            mRNA sequence.
ACCESSION   CC798987
VERSION     CC798987.2  GI:46014580
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   BayGenomics.
  TITLE     http://baygenomics.ucsf.edu/
  JOURNAL   Unpublished (2001)
COMMENT     On Apr 1, 2004 this sequence version replaced gi:32394210.
            Contact: BayGenomics
            Bay Area Functional Genomics Consortium (BayGenomics)
            Email: info@baygenomics.ucsf.edu
            Sequence tag generated by 5' RACE of total RNA from gene trap ES
            cell line. ES cell lines harboring insertion mutation of target
            gene are available upon request from BayGenomics. Annotation
            information available from
            http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?
            OPTION=EXACT&TYPE=CELL_LINE&KEY=RRK477
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129 ola"
                     /db_xref="taxon:10090"
                     /sex="Male"
                     /cell_type="Embryonic stem cell"
                     /clone_lib="BayGenomics Gene Trap Library pGT2Lxf"
                     /note="Vector: pGT2Lxf"
ORIGIN

  Query Match             73.8%;  Score 11.8;  DB 9;  Length 46;
  Best Local Similarity   86.7%;  Pred. No. 2.1e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 AAGCCACCCAAGGCA 16
              ||| ||||||| |||
Db         14 AAGTCACCCAAAGCA 28


RESULT 6
AU104174
LOCUS       AU104174                 50 bp    mRNA    linear   EST 28-JAN-2004
DEFINITION  AU104174 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            HEP09604, mRNA sequence.
ACCESSION   AU104174
VERSION     AU104174.1  GI:13553695
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
  MEDLINE   21270072
    PUBMED  11375929
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HEP09604"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN

  Query Match             73.8%;  Score 11.8;  DB 1;  Length 50;
  Best Local Similarity   86.7%;  Pred. No. 2.1e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 AAGCCACCCAAGGCA 16
              |||  ||||||||||
Db         31 AAGTTACCCAAGGCA 45


RESULT 7
CO794661
LOCUS       CO794661                 20 bp    mRNA    linear   EST 05-AUG-2004
DEFINITION  NT144B_A07 St18-22 Neural tube (NT) Ambystoma mexicanum cDNA 5'
            similar to hypothetical protein, mRNA sequence.
ACCESSION   CO794661
VERSION     CO794661.1  GI:51010632
KEYWORDS    EST.
SOURCE      Ambystoma mexicanum (axolotl)
  ORGANISM  Ambystoma mexicanum
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
            Ambystoma.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Habermann,B., Bebin,A.G., Herklotz,S., Volkmer,M., Eckelt,K.,
            Pehlke,K., Epperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,E.M.
  TITLE     An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
            expressed sequence tags from embryonic and regenerating blastema
            cDNA libraries
  JOURNAL   Genome Biol. (2004) In press
COMMENT     Contact: Elly M. Tanaka
            Tanaka Lab
            Max Planck Institute of Molecular Cell Biology and Genetics,
            Dresden
            Pfotenhauerstrasse 108,01307 Dresden, Germany
            Tel: 0049 351 210 2620
            Fax: 0049 351 210 1489
            Email: tanaka@mpi-cbg.de
            Plate: NT144B  row: 07  column: A
            Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Ambystoma mexicanum"
                     /mol_type="mRNA"
                     /db_xref="taxon:8296"
                     /tissue_type="Neural Tube, Notochord, Somites"
                     /cell_type="Includes Neural tube, notochord, somites"
                     /dev_stage="Stage 18-22"
                     /clone_lib="St18-22 Neural tube (NT)"
                     /note="Vector: pCMVSport6; Site_1: NotI; Site_2: SalI;
                     Unnormalized cDNA plasmid library prepared by Invitrogen.
                     Size fractionated mRNA was polydT primed and cloned into
                     NotI-SalI site of pCMVSport6. Bacterial host is
                     EMDH10B-TONA. Average insert size is 1.5 kB.
                     TAG_LIB=NT"
```

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ORIGIN

  Query Match             70.0%;  Score 11.2;  DB 7;  Length 20;
  Best Local Similarity   81.2%;  Pred. No. 4e+05;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              |||| || ||||||  |
Db          1 AAAGGCAGCCAAGGTA 16


RESULT 8
BX567608
LOCUS       BX567608                 35 bp    mRNA    linear   EST 14-OCT-2003
DEFINITION  BX567608 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse89a03_p1c, mRNA sequence.
ACCESSION   BX567608
VERSION     BX567608.1  GI:33434526
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse89a03_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"
ORIGIN

  Query Match             70.0%;  Score 11.2;  DB 5;  Length 35;
  Best Local Similarity   81.2%;  Pred. No. 4.2e+05;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              |||||||  ||| |||
Db          8 AAAGCCATACAATGCA 23


RESULT 9
AZ505596/c
LOCUS       AZ505596                 36 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0346B24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0346B24 F, genomic survey sequence.
ACCESSION   AZ505596
VERSION     AZ505596.1  GI:10686912
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0346  row: B  column: 24
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 36.
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0346B24"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             70.0%;  Score 11.2;  DB 8;  Length 36;
  Best Local Similarity   81.2%;  Pred. No. 4.2e+05;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              |||||  || |||  |||
Db         19 AAAGCAACACAAAGCA 4


RESULT 10
AI597737
LOCUS       AI597737                 37 bp    mRNA    linear   EST 21-APR-1999
DEFINITION  tu91b01.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2258377 3'
            similar to TR:Q08805 Q08805 SALIVARY PROLINE-RICH PROTEIN L ;, mRNA
```

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            sequence.
ACCESSION   AI597737
VERSION     AI597737.1  GI:4606785
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .37
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2258377"
                      /tissue_type="poorly differentiated adenocarcinoma with
                      signet ring cell features"
                      /lab_host="DH10B"
                      /clone_lib="NCI_CGAP_Gas4"
                      /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI;
                      Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 1.69 kb. Life Technologies catalog #:
                      11549-011"
ORIGIN

  Query Match             70.0%;  Score 11.2;  DB 1;  Length 37;
  Best Local Similarity   81.2%;  Pred. No. 4.2e+05;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              | ||||  |||||||  |
Db          8 AGAGCCCCCCAAGGGA 23


RESULT 11
BF211603
LOCUS       BF211603                37 bp    mRNA    linear   EST 06-NOV-2000
DEFINITION  601812103F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4046569 5',
            mRNA sequence.
ACCESSION   BF211603
VERSION     BF211603.1  GI:11105189
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM874  row: e  column: 02
            High quality sequence stop: 37.
FEATURES              Location/Qualifiers
     source           1. .37
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:4046569"
                      /tissue_type="from chronic myelogenous leukemia"
                      /lab_host="DH10B (T1 phage-resistant)"
                      /clone_lib="NIH_MGC_54"
                      /note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
                      Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI
                      (ggccattatggcc); Double-stranded cDNA was prepared from
                      cell line RNA.  5' and 3' adaptors were used in cloning as
                      follows: 5' adaptor sequence:  5'-CACGGCCATTATGGCC-3' and
                      3' adaptor sequence:
                      5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                      C, or G and N = A, C,  G, or T).  Average insert size
                      1.75 kb (range 0.9-4.0 kb).  15/15 colonies contained
                      inserts by PCR. This library was enriched for full-length
                      clones and was constructed by Clontech  Laboratories (Palo
                      Alto, CA)."
ORIGIN

  Query Match             70.0%;  Score 11.2;  DB 2;  Length 37;
  Best Local Similarity   81.2%;  Pred. No. 4.2e+05;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              | ||||  |||||||  |
Db          3 AGAGCCCCCCAGGAA 18


RESULT 12
AI690571
LOCUS       AI690571                40 bp    mRNA    linear   EST 27-MAY-1999
DEFINITION  tq02a02.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2207594 3'
            similar to TR:O63545 O63545 NADH DEHYDROGENASE SUBUNIT 5 ;, mRNA
            sequence.
ACCESSION   AI690571
VERSION     AI690571.1  GI:4901873
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .40
                      /organism="Homo sapiens"
```

```
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2207594"
                     /tissue_type="poorly-differentiated endometrial
                     adenocarcinoma, 2 pooled tumors"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Ut3"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.45 kb. Life Technologies catalog #:
                     11541-018"
ORIGIN

  Query Match             70.0%;  Score 11.2;  DB 1;  Length 40;
  Best Local Similarity   81.2%;  Pred. No. 4.3e+05;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||| ||||||||  ||
Db          5 AAACCCACCCAACACA 20


RESULT 13
R50470/c
LOCUS       R50470                    43 bp    mRNA    linear   EST 18-MAY-1995
DEFINITION  yj56h09.r1 Soares breast 2NbHBst Homo sapiens cDNA clone
            IMAGE:152801 5' similar to SP:ATPQ_BOVIN P13620 ATP SYNTHASE D
            CHAIN, MITOCHONDRIAL ;, mRNA sequence.
ACCESSION   R50470
VERSION     R50470.1  GI:812372
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence starts: 1
            High quality sequence stops: 1
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Possible reversed clone: similarity on wrong strand
            Seq primer: M13RP1
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:565050"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:152801"
                     /sex="Female"
                     /dev_stage="adult"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares breast 2NbHBst"
                     /note="Organ: breast; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of a modified pT7T3 vector (Pharmacia).
                     Library went through one round of normalization to a Cot =
                     230. Library constructed by Bento Soares and M.Fatima
                     Bonaldo."
ORIGIN

  Query Match             70.0%;  Score 11.2;  DB 7;  Length 43;
  Best Local Similarity   81.2%;  Pred. No. 4.3e+05;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              ||||| |||| || ||
Db         43 AAAGCTACCCCAGTCA 28


RESULT 14
AI355812
LOCUS       AI355812                  46 bp    mRNA    linear   EST 04-JAN-1999
DEFINITION  qt94h07.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:1962973 3'
            similar to SW:PRP2_HUMAN P02812 SALIVARY PROLINE-RICH PROTEIN
            PRECURSOR ;, mRNA sequence.
ACCESSION   AI355812
VERSION     AI355812.1  GI:4095965
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1962973"
                     /tissue_type="moderately-differentiated adenocarcinoma"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Co14"
                     /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.7 kb. Life Technologies catalog #:
                     11531-019"
ORIGIN

  Query Match             70.0%;  Score 11.2;  DB 1;  Length 46;
  Best Local Similarity   81.2%;  Pred. No. 4.3e+05;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              || |||||||| | ||
Db         28 AACGCCACCCACGACA 43


RESULT 15
```

```
R78378
LOCUS       R78378                  46 bp    mRNA    linear   EST 07-JUN-1995
DEFINITION  yi78d11.s1 Soares placenta Nb2HP Homo sapiens cDNA clone
            IMAGE:145365 3' similar to gb:D11428 PERIPHERAL MYELIN PROTEIN 22
            (HUMAN);, mRNA sequence.
ACCESSION   R78378
VERSION     R78378.1  GI:853488
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 702
            High quality sequence starts: 1
            High quality sequence stops: 1
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Insert Length: 702   Std Error: 0.00
            Seq primer: Promega -21m13
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:563967"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:145365"
                     /sex="Female"
                     /dev_stage="placenta obtained at birth (full term)"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares placenta Nb2HP"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo.  "
ORIGIN

  Query Match            70.0%;  Score 11.2;  DB 7;  Length 46;
  Best Local Similarity  81.2%;  Pred. No. 4.3e+05;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAAGCCACCCAAGGCA 16
              || |||||||| | ||
Db         29 AAGGCCACCCAGGCCA 44


Search completed: March 29, 2005, 09:34:07
Job time : 1835 secs
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